

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 101.rai.

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This page gives you Search Results detail for the Application 10717243 and Search Result us-10-717-243-101.rai.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:37:31 ; Search time 33.8063 Seconds
(without alignments)
649.885 Million cell updates/sec

Title: US-10-717-243-101
Perfect score: 1277
Sequence: 1 GLDTVSFSTKGATYITYVNF.....AVDQVKPKIALLKFVDKDPK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:
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6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1277	100.0	251	1	US-08-425-336-101	Sequence 101, App
2	1277	100.0	251	1	US-08-488-113B-101	Sequence 101, App
3	1277	100.0	251	1	US-08-477-484B-101	Sequence 101, App
4	1277	100.0	251	1	US-08-646-360-101	Sequence 101, App
5	1277	100.0	251	2	US-08-839-765-101	Sequence 101, App
6	1277	100.0	251	2	US-09-136-389-101	Sequence 101, App
7	1277	100.0	251	2	US-09-610-838-101	Sequence 101, App
8	1277	100.0	251	2	US-09-711-485-101	Sequence 101, App
9	1273	99.7	251	1	US-08-425-336-99	Sequence 99, Appl
10	1273	99.7	251	1	US-08-425-336-100	Sequence 100, App

11	1273	99.7	251	1	US-08-488-113B-99	Sequence 99, Appl
12	1273	99.7	251	1	US-08-488-113B-100	Sequence 100, App
13	1273	99.7	251	1	US-08-477-484B-99	Sequence 99, Appl
14	1273	99.7	251	1	US-08-477-484B-100	Sequence 100, App
15	1273	99.7	251	1	US-08-646-360-99	Sequence 99, Appl
16	1273	99.7	251	1	US-08-646-360-100	Sequence 100, App
17	1273	99.7	251	2	US-08-839-765-99	Sequence 99, Appl
18	1273	99.7	251	2	US-08-839-765-100	Sequence 100, App
19	1273	99.7	251	2	US-09-136-389-99	Sequence 99, Appl
20	1273	99.7	251	2	US-09-136-389-100	Sequence 100, App
21	1273	99.7	251	2	US-09-610-838-99	Sequence 99, Appl
22	1273	99.7	251	2	US-09-610-838-100	Sequence 100, App
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24	1273	99.7	251	2	US-09-711-485-100	Sequence 100, App
25	1269	99.4	251	1	US-08-425-336-2	Sequence 2, Appli
26	1269	99.4	251	1	US-08-425-336-110	Sequence 110, App
27	1269	99.4	251	1	US-08-488-113B-2	Sequence 2, Appli
28	1269	99.4	251	1	US-08-488-113B-110	Sequence 110, App
29	1269	99.4	251	1	US-08-477-484B-2	Sequence 2, Appli
30	1269	99.4	251	1	US-08-477-484B-110	Sequence 110, App
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32	1269	99.4	251	1	US-08-646-360-110	Sequence 110, App
33	1269	99.4	251	1	US-08-621-803-247	Sequence 247, App
34	1269	99.4	251	2	US-08-839-765-2	Sequence 2, Appli
35	1269	99.4	251	2	US-08-839-765-110	Sequence 110, App
36	1269	99.4	251	2	US-09-136-389-2	Sequence 2, Appli
37	1269	99.4	251	2	US-09-136-389-110	Sequence 110, App
38	1269	99.4	251	2	US-09-217-352-247	Sequence 247, App
39	1269	99.4	251	2	US-09-610-838-2	Sequence 2, Appli
40	1269	99.4	251	2	US-09-610-838-110	Sequence 110, App
41	1269	99.4	251	2	US-09-711-485-2	Sequence 2, Appli
42	1269	99.4	251	2	US-09-711-485-110	Sequence 110, App
43	1269	99.4	251	2	US-09-645-603B-2	Sequence 2, Appli
44	1266	99.1	251	1	US-07-901-707-2	Sequence 2, Appli
45	1266	99.1	251	1	US-07-988-430-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
 US-08-425-336-101
; Sequence 101, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60

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Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 2
US-08-488-113B-101
; Sequence 101, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60

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Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 3

US-08-477-484B-101
; Sequence 101, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336

; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-484B-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHIGPLLRKKADDPGKAFVLVALSNDN 60

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Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 4
US-08-646-360-101
; Sequence 101, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-646-360-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180
Qy	181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMSEAVELERANGKKYYVTAVDQVKPKI 240
Db	181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMSEAVELERANGKKYYVTAVDQVKPKI 240
Qy	241 ALLKFVDKDPK 251
Db	241 ALLKFVDKDPK 251

RESULT 5

US-08-839-765-101
; Sequence 101, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago

; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-839-765-101

Query Match 100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 1 GLDTVSFSTKGATITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 6
US-09-136-389-101
; Sequence 101, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-136-389-101

Query Match 100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.e-118;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 7
US-09-610-838-101
; Sequence 101, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-610-838-101

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Query Match          100.0%;  Score 1277;  DB 2;  Length 251;
Best Local Similarity 100.0%;  Pred. No. 1.e-118;
Matches 251;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Y      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRRKKADDPGKAFVLVALSNND 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Y      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRRKKADDPGKAFVLVALSNND 60

Y      61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Y      61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Y      121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASLLVVIQMVEAARFTFIENQIRNN 180

```

Db 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180
Qy 181 FQQRIRPANNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 8
US-09-711-485-101
; Sequence 101, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA;
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-711-485-101

Query Match 100.08; Score 1277; DB 2; Length 251;
Best Local Similarity 100.08; Pred. No. 1.1e-118;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
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Db      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Qy      61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db      61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Qy      121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db      121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Qy      181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db      181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Qy      241 ALLKFVDKDPK 251
Db      241 ALLKFVDKDPK 251

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RESULT 9

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US-08-425-336-99
; Sequence 99, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
;   APPLICANT: Better, Marc D.
;   APPLICANT: Carroll, Stephen F.
;   APPLICANT: Studnika, Gary M.
;   TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
;   TITLE OF INVENTION: Proteins
;   NUMBER OF SEQUENCES: 140
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;     STREET: 6300 Sears Tower, 233 South Wacker Drive
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: USA
;     ZIP: 60606-6402
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/425,336
;   FILING DATE: 18-APR-1995
;   CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/064,691
;   FILING DATE: 12-MAY-1993
;   APPLICATION NUMBER: US 07/901,707
;   FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/787,567
;   FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Meyers, Thomas C.
;   REGISTRATION NUMBER: P-36,989
;   REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312/474-6300
;   TELEFAX: 312/474-0448
;   TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 99:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 251 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-425-336-99

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Query Match          99.7%;  Score 1273;  DB 1;  Length 251;
Best Local Similarity 99.6%;  Pred. No. 2.7e-118;
Matches 250;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db      61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

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Db      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Qy      61 GQLAEIAIDVTSVYVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db      61 GQLAEIAIDVTSVYVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Qy      121 AYRETTDLGIEPLRIGIKLKDENAIDNYKPTEIASSLLVVIQMVEAARFTFIENQIRNN 180
Db      121 AYRETTDLGIEPLRIGIKLKDENAIDNYKPTEIASSLLVVIQMVEAARFTFIENQIRNN 180
Qy      181 FQQRIRPANNTISLENKGWLKFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db      181 FQQRIRPANNTISLENKGWLKFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Qy      241 ALLKFVDKDPK 251
Db      241 ALLKFVDKDPK 251

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RESULT 10

US-08-425-336-100

; Sequence 100, Application US/08425336

; Patent No. 5621083

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 100:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-425-336-100

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Query Match          99.7%;  Score 1273;  DB 1;  Length 251;
Best Local Similarity 99.6%;  Pred. No. 2.7e-118;
Matches 250;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
      |||||||...|||||...|||||...|||||...|||||...|||||...|||||...|||...|||...|||...

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Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKCFVLVALSNDN 60
Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 11

US-08-488-113B-99
; Sequence 99, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-99

Query Match 99.7%; Score 1273; DB 1; Length 251;
 Best Local Similarity 99.6%; Pred. No. 2.7e-118;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
 |||||||
 Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKCDDPGKAFVLVALSNDN 60

 Qy 61 GQLAEIAIDVTSVYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHF GG SYP SLEGEK 120
 |||||||
 Db 61 GQLAEIAIDVTSVYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHF GG SYP SLEGEK 120

 Qy 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQM VSEAARFTFIENQIRNN 180
 |||||||
 Db 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQM VSEAARFTFIENQIRNN 180

 Qy 181 FQQRIRPANNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
 |||||||
 Db 181 FQQRIRPANNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

 Qy 241 ALLKFVDKDPK 251
 |||||||
 Db 241 ALLKFVDKDPK 251

RESULT 12

US-08-488-113B-100
 ; Sequence 100, Application US/08488113B
 ; Patent No. 5744580
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; TITLE OF INVENTION: Proteins
 ; NUMBER OF SEQUENCES: 169
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/488,113B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/425,336
 ; FILING DATE: 18-APR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8889
 ; TELEFAX: 312/707-9155
 ; TELEX: 650 388-1248

; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-100

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKADDPGKAFVLVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKADDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFHGGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFHGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQM VSEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQM VSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 13

US-08-477-484B-99

; Sequence 99, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:

; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-484B-99

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKAFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANN TISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANN TISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 14
US-08-477-484B-100
; Sequence 100, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-484B-100

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 121 AYRETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLVVIQMVEARFTFIENQIRNN 180
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Db 181 FQQRIRPANNNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 15

US-08-646-360-99

; Sequence 99, Application US/08646360

; Patent No. 5837491

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; TITLE OF INVENTION: Proteins

; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

; STREET: 500 West Madison Street, 34th floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/646,360

; FILING DATE: 13-MAY-1996

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/05348

; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-360-99

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKAFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

Search completed: July 20, 2006, 09:38:57
Job time : 34.8063 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 101.rapbm.

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This page gives you Search Results detail for the Application 10717243 and Search Result us-10-717-243-101.rapbm.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:40:12 ; Search time 81.5055 Seconds
(without alignments)
1426.491 Million cell updates/sec

Title: US-10-717-243-101
Perfect score: 1277
Sequence: 1 GLDTVSFSTKGATYITYVNF.....AVDQVKPKIALLKFVDKDPK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:
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5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1277	100.0	251	5	US-10-717-243-101	Sequence 101, App
3	1273	99.7	251	4	US-10-127-890-99	Sequence 99, Appl
4	1273	99.7	251	4	US-10-127-890-100	Sequence 100, App
5	1273	99.7	251	5	US-10-717-243-99	Sequence 99, Appl
6	1273	99.7	251	5	US-10-717-243-100	Sequence 100, App
7	1269	99.4	251	3	US-09-765-527-247	Sequence 247, App
8	1269	99.4	251	4	US-10-127-890-2	Sequence 2, Appli
9	1269	99.4	251	4	US-10-127-890-110	Sequence 110, App
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11	1269	99.4	251	5	US-10-717-243-110	Sequence 110, App

12	1269	99.4	316	4	US-10-074-596-1	Sequence 1, Appli
13	1269	99.4	498	5	US-10-964-195-13	Sequence 13, Appl
14	1269	99.4	507	4	US-10-074-596-11	Sequence 11, Appl
15	1266	99.1	293	3	US-09-765-527-259	Sequence 259, App
16	1266	99.1	309	3	US-09-765-527-253	Sequence 253, App
17	1266	99.1	332	3	US-09-765-527-251	Sequence 251, App
18	1265	99.1	751	6	US-11-084-080-26	Sequence 26, Appl
19	1264	99.0	251	4	US-10-127-890-108	Sequence 108, App
20	1264	99.0	251	5	US-10-717-243-108	Sequence 108, App
21	1261	98.7	251	4	US-10-127-890-103	Sequence 103, App
22	1261	98.7	251	4	US-10-127-890-104	Sequence 104, App
23	1261	98.7	251	4	US-10-127-890-105	Sequence 105, App
24	1261	98.7	251	4	US-10-127-890-106	Sequence 106, App
25	1261	98.7	251	4	US-10-127-890-109	Sequence 109, App
26	1261	98.7	251	5	US-10-717-243-103	Sequence 103, App
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28	1261	98.7	251	5	US-10-717-243-105	Sequence 105, App
29	1261	98.7	251	5	US-10-717-243-106	Sequence 106, App
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31	1260	98.7	251	4	US-10-127-890-102	Sequence 102, App
32	1260	98.7	251	4	US-10-127-890-107	Sequence 107, App
33	1260	98.7	251	4	US-10-127-890-111	Sequence 111, App
34	1260	98.7	251	5	US-10-717-243-102	Sequence 102, App
35	1260	98.7	251	5	US-10-717-243-107	Sequence 107, App
36	1260	98.7	251	5	US-10-717-243-111	Sequence 111, App
37	1212.5	94.9	513	5	US-10-926-731A-12	Sequence 12, Appl
38	1201	94.0	506	5	US-10-964-195-11	Sequence 11, Appl
39	348	27.3	263	4	US-10-127-890-4	Sequence 4, Appli
40	348	27.3	263	5	US-10-717-243-4	Sequence 4, Appli
41	346	27.1	267	4	US-10-282-935-1	Sequence 1, Appli
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44	346	27.1	267	5	US-10-717-243-1	Sequence 1, Appli
45	346	27.1	268	6	US-11-010-795-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1
 US-10-127-890-101
 ; Sequence 101, Application US/10127890
 ; Publication No. US20030166196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; Carroll, Stephen F.
 ; Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
 ; NUMBER OF SEQUENCES: 173
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/127,890
 ; FILING DATE: 23-Apr-2002
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/646,360
 ; FILING DATE: 13-MAY-1996
 ; APPLICATION NUMBER: PCT/US94/05348
 ; FILING DATE: 12-MAY-1994
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; APPLICATION NUMBER: US 07/901,707

RESULT 2
US-10-717-243-101
; Sequence 101, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-717-243-101

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Query Match          100.0%; Score 1277; DB 5; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e-115;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-10-127-890-99
; Sequence 99, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; ; Carroll, Stephen F.
; ; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890

; FILING DATE: 23-Apr-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-127-890-99

Query Match 99.7%; Score 1273; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.3e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 181 FQQRIRPANN TISLENKWGKLSFQIRTS GANGMFSEAVELERANGKYYVTAVDQVKPKI 240
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Qy 241 ALLKFVDKDPK 251
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Db 241 ALLKFVDKDPK 251

RESULT 4
US-10-127-890-100
; Sequence 100, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
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; ZIP: 60661
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
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; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-127-890-100

Query Match 99.7%; Score 1273; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.3e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
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Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180
|||||||||||||||||||||||||||||||||||||||||
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
|||||||||||||||||||||||||||||||||||||||||
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
|||||||||||
Db 241 ALLKFVDKDPK 251

RESULT 5
US-10-717-243-99
; Sequence 99, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:

LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 99:

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Query Match          99.7%; Score 1273; DB 5; Length 251; .
Best Local Similarity 99.6%; Pred. No. 3.3e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLRLKKADDPGKAFVLVALSNND 60
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLRLKKCDDPGKAFVLVALSNND 60

Qy      61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy      121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180

Qy      181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 240
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 240

Qy      241 ALLKFVDKDPK 251
        ||||||| | | |
Db      241 ALLKFVDKDPK 251

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RESULT 6
US-10-717-243-100
: Sequence 100, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.

; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-717-243-100

Query Match 99.7%; Score 1273; DB 5; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.3e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 7

US-09-765-527-247
; Sequence 247, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-765-527-247

Query Match 99.4%; Score 1269; DB 3; Length 251;
Best Local Similarity 99.2%; Pred. No. 8e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVILVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKCFVILVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFEGGSYPSEGEK 120
Db 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFEGGSYPSEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 8
US-10-127-890-2
; Sequence 2, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-127-890-2

Query Match 99.4%; Score 1269; DB 4; Length 251;
Best Local Similarity 99.2%; Pred. No. 8e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 1 GLDTVSFSTKGATITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFVGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFVGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANN TISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANN TISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 9
US-10-127-890-110

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; Sequence 110, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
;   APPLICANT: Better, Marc D.
;             Carroll, Stephen F.
;             Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                     Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;   STREET: 500 West Madison Street, 34th floor
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60661
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/127,890
;   FILING DATE: 23-Apr-2002
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/646,360
;   FILING DATE: 13-MAY-1996
;   APPLICATION NUMBER: PCT/US94/05348
;   FILING DATE: 12-MAY-1994
;   APPLICATION NUMBER: US 08/064,691
;   FILING DATE: 12-MAY-1993
;   APPLICATION NUMBER: US 07/988,430
;   FILING DATE: 09-DEC-1992
;   APPLICATION NUMBER: US 07/901,707
;   FILING DATE: 19-JUN-1992
;   APPLICATION NUMBER: US 07/787,567
;   FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: McNicholas, Janet M.
;   REGISTRATION NUMBER: 32,918
;   REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312/707-8889
;   TELEFAX: 312/707-9155
;   TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 110:
;   .SEQUENCE CHARACTERISTICS:
;     LENGTH: 251 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;   .SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-127-890-110

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Query Match          99.4%;  Score 1269;  DB 4;  Length 251;
Best Local Similarity 99.6%;  Pred. No. 8e-115;
Matches 250;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy      1 GLDTVSFSTKGATIYTIVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
        ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||
Db      1 GLDTVSFSTCGATIYTIVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60

Qy      61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFVGSYPSLEGEK 120
        ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||
Db      61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFVGSYPSLEGEK 120

Qy      121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVEAARFTFIENQIRNN 180
        ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||
Db      121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVEAARFTFIENQIRNN 180

Qy      181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
        ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||
Db      181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy      241 ALLKFVDKDPK 251

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|||||||||||
Db 241 ALLKFVDKDPK 251

RESULT 10
US-10-717-243-2
; Sequence 2, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-717-243-2

Query Match 99.4%; Score 1269; DB 5; Length 251;
Best Local Similarity 99.2%; Pred. No. 8e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
|||
Db 1 GLDTVSFSTKGATITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFVGSYPSLEGEK 120
|||
Db 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFVGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
|||
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 11
US-10-717-243-110
; Sequence 110, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-717-243-110

Query Match 99.4%; Score 1269; DB 5; Length 251;
Best Local Similarity 99.6%; Pred. No. 8e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 1 GLDTVSFSTCGATITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

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Db      61 GQLAEIAIDVTSVYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFHGGSPSLEGEK 120
Qy      121 AYRETTDLGIEPLRIGIKKKDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db      121 AYRETTDLGIEPLRIGIKKKDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Qy      181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db      181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Qy      241 ALLKFVDKDPK 251
Db      241 ALLKFVDKDPK 251

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RESULT 12

US-10-074-596-1

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; Sequence 1, Application US/10074596
; Publication No. US20030176331A1
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MICHAEL G.
; APPLICANT: CHEUNG, LAWRENCE
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
; TITLE OF INVENTION: MAKING THEEOF
; FILE REFERENCE: CLFR:007US
; CURRENT APPLICATION NUMBER: US/10/074,596
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,402
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Gelsonium multiflorum
US-10-074-596-1

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Query Match          99.4%;  Score 1269;  DB 4;  Length 316;
Best Local Similarity 99.2%;  Pred. No. 1.1e-114;
Matches 249;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;
Qy      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVIVALSDND 60
Db      47 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVIVALSDND 106
Qy      61 GQLAEIAIDVTSVYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFHGGSPSLEGEK 120
Db      107 GQLAEIAIDVTSVYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFHGGSPSLEGEK 166
Qy      121 AYRETTDLGIEPLRIGIKKKDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db      167 AYRETTDLGIEPLRIGIKKKDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 226
Qy      181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db      227 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 286
Qy      241 ALLKFVDKDPK 251
Db      287 ALLKFVDKDPK 297

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RESULT 13

US-10-964-195-13

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; Sequence 13, Application US/10964195
; Publication No. US20050163774A1
; GENERAL INFORMATION:
; APPLICANT: Rosenblum et al.
; TITLE OF INVENTION: Immunotoxins Directed Against c-erbB-2 (HER-2/Neu)
; TITLE OF INVENTION: Related Surface Antigens
; FILE REFERENCE: D5425CIP2
; CURRENT APPLICATION NUMBER: US/10/964,195
; CURRENT FILING DATE: 2004-10-13
; PRIOR APPLICATION NUMBER: US/09/320,156
; PRIOR FILING DATE: 1999-05-26

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; PRIOR APPLICATION NUMBER: 08/404,499
; PRIOR FILING DATE: 1995-03-17
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 13
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Polypeptide encoded by the scFv23-gelonin immunotoxin
US-10-964-195-13

Query Match 99.4%; Score 1269; DB 5; Length 498;
Best Local Similarity 99.2%; Pred. No. 2.1e-114;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 247 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKCFVLVALSNDN 306

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
Db 307 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 366

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVEAARFTFIENQIRNN 180
Db 367 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVEAARFTFIENQIRNN 426

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 427 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 486

Qy 241 ALLKFVDKDPK 251
Db 487 ALLKFVDKDPK 497

RESULT 14
US-10-074-596-11
; Sequence 11, Application US/10074596
; Publication No. US20030176331A1
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MICHAEL G.
; APPLICANT: CHEUNG, LAWRENCE
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
; TITLE OF INVENTION: MAKING THEEOF
; FILE REFERENCE: CLFR:007US
; CURRENT APPLICATION NUMBER: US/10/074,596
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,402
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-074-596-11

Query Match 99.4%; Score 1269; DB 4; Length 507;
Best Local Similarity 99.2%; Pred. No. 2.1e-114;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 257 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKCFVLVALSNDN 316

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
Db 317 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 376

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVEAARFTFIENQIRNN 180
Db 377 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVEAARFTFIENQIRNN 436

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Qy      181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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Db      437 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 496

Qy      241 ALLKFVDKDPK 251
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Db      497 ALLKFVDKDPK 507

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RESULT 15

US-09-765-527-259

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; Sequence 259, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
;   APPLICANT: Better, Marc D.
;   TITLE OF INVENTION: Methods for Recombinant Microbial Production of
;                      Fusion Proteins and BPI-Derived Peptides
;   NUMBER OF SEQUENCES: 265
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;     STREET: 6300 Sears Tower, 233 South Wacker Drive
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: United States of America
;     ZIP: 60606-6402
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/765,527
;   FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/621,803
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Borun, Michael F.
;   REGISTRATION NUMBER: 25,447
;   REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312/474-6300
;   TELEFAX: 312/474-0448
;   TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 259:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 293 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 259:

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US-09-765-527-259

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Query Match          99.1%;  Score 1266;  DB 3;  Length 293;
Best Local Similarity 98.8%;  Pred. No. 2e-114;
Matches 248;  Conservative 1;  Mismatches 2;  Indels 0;  Gaps 0;

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Qy      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
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Db      23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLPKKCDDPGKCFVLVALSNDN 82

Qy      61 GQLAEIAIDVTSVVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
       |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db      83 GQLAEIAIDVTSVVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSEGEK 142

Qy      121 AYRETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
       |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db      143 AYRETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 202

Qy      181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
       |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db      203 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 262

Qy      241 ALLKFVDKDPK 251
       |||||||:|||||||
Db      263 ALLKFVDKDPK 273

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Job time : 81.5055 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 101.rapbn.

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start

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:40:39 ; Search time 14.8192 Seconds
(without alignments)
976.754 Million cell updates/sec

Title: US-10-717-243-101
Perfect score: 1277
Sequence: 1 GLDTVVSFSTKGATYITVYNE.....AVDOVKPKTIALIKEVVDKDPK 251

Scoring table: BLOSUM62
Gapopen 10.0 , Gapext 0.5

Searched: 208217 segs. 57668156 residues

Total number of hits satisfying chosen parameters: 208217

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Query						Description
	Score	Match	Length	DB	ID		
1	346	27.1	267	7	US-11-263-537-1		Sequence 1, Appli
2	315	24.7	251	7	US-11-263-537-3		Sequence 3, Appli
3	128.5	10.1	282	6	US-10-449-902-56587		Sequence 56587, A
4	111.5	8.7	277	6	US-10-953-349-30545		Sequence 30545, A
5	111.5	8.7	277	7	US-11-056-355B-61236		Sequence 61236, A
6	111.5	8.7	281	6	US-10-953-349-30544		Sequence 30544, A
7	111.5	8.7	281	7	US-11-056-355B-61235		Sequence 61235, A
8	111.5	8.7	298	6	US-10-953-349-30543		Sequence 30543, A
9	111.5	8.7	298	7	US-11-056-355B-61234		Sequence 61234, A

10	110	8.6	298	6	US-10-449-902-39064	Sequence 39064, A
11	108.5	8.5	232	6	US-10-953-349-10528	Sequence 10528, A
12	108.5	8.5	245	6	US-10-953-349-10527	Sequence 10527, A
13	108.5	8.5	252	6	US-10-953-349-10526	Sequence 10526, A
14	95	7.4	876	6	US-10-471-571A-5500	Sequence 5500, Ap
15	89.5	7.0	296	6	US-10-449-902-41985	Sequence 41985, A
16	88.5	6.9	239	6	US-10-953-349-14022	Sequence 14022, A
17	88.5	6.9	239	7	US-11-056-355B-55899	Sequence 55899, A
18	88.5	6.9	248	6	US-10-953-349-14021	Sequence 14021, A
19	88.5	6.9	248	7	US-11-056-355B-55898	Sequence 55898, A
20	88.5	6.9	254	6	US-10-953-349-14020	Sequence 14020, A
21	88.5	6.9	254	7	US-11-056-355B-55897	Sequence 55897, A
22	87	6.8	767	6	US-10-449-902-56749	Sequence 56749, A
23	85	6.7	291	6	US-10-449-902-37995	Sequence 37995, A
24	84.5	6.6	219	6	US-10-953-349-5981	Sequence 5981, Ap
25	84.5	6.6	219	7	US-11-056-355B-23415	Sequence 23415, A
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27	84.5	6.6	219	7	US-11-056-355B-28637	Sequence 28637, A
28	84.5	6.6	219	7	US-11-056-355B-32227	Sequence 32227, A
29	84.5	6.6	219	7	US-11-056-355B-40030	Sequence 40030, A
30	84.5	6.6	219	7	US-11-056-355B-100712	Sequence 100712,
31	84.5	6.6	219	7	US-11-056-355B-111951	Sequence 111951,
32	84.5	6.6	260	6	US-10-953-349-5980	Sequence 5980, Ap
33	84.5	6.6	260	7	US-11-056-355B-23414	Sequence 23414, A
34	84.5	6.6	260	7	US-11-056-355B-24651	Sequence 24651, A
35	84.5	6.6	260	7	US-11-056-355B-28636	Sequence 28636, A
36	84.5	6.6	260	7	US-11-056-355B-32226	Sequence 32226, A
37	84.5	6.6	260	7	US-11-056-355B-40029	Sequence 40029, A
38	84.5	6.6	260	7	US-11-056-355B-100711	Sequence 100711,
39	84.5	6.6	260	7	US-11-056-355B-111950	Sequence 111950,
40	84.5	6.6	278	6	US-10-953-349-5979	Sequence 5979, Ap
41	84.5	6.6	278	7	US-11-056-355B-23413	Sequence 23413, A
42	84.5	6.6	278	7	US-11-056-355B-24650	Sequence 24650, A
43	84.5	6.6	278	7	US-11-056-355B-28635	Sequence 28635, A
44	84.5	6.6	278	7	US-11-056-355B-32225	Sequence 32225, A
45	84.5	6.6	278	7	US-11-056-355B-40028	Sequence 40028, A

ALIGNMENTS

RESULT 1
US-11-263-537-1
; Sequence 1, Application US/11263537
; Publication No. US20060100135A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
; TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
; FILE REFERENCE: UTSD:884USC1
; CURRENT APPLICATION NUMBER: US/11/263,537
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: 10/282,935
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-263-537-1

Query Match 27.1%; Score 346; DB 7; Length 267;
Best Local Similarity 36.8%; Pred. No. 2.6e-23;
Matches 93; Conservative 45; Mismatches 99; Indels 16; Gaps 9;

Qy 5 VSFSTKGATYITYVNFLNELRVKLKPEGN-SHGIPLLRKKADDP-GKAFVLVALSNDNGQ 62
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 Db 9 INFTTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68

 Qy 63 LAEIAIDVTSVYVVGYQVRNRNSYFFKDAPD----AAYEGLFKNTIKTR--LHFGGSYPS 115
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 Db 69 SVTLALDVTNAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRYTFAFGGNYDR 125

 Qy 116 LEGEKA-YRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLIVVIQMVSEAARFTFIE 174
 ||| :||| :||| ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 126 LEQLAGNLRENIELNGNPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 185

 Qy 175 NQIRN--NFQQRIRPANNNTISLENKWKGLSFQIRTSGANGMFSEAVELERANGKYYVTA 232
 ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 186 GEMRTRIRYNRRSAPDPSVITLENSWGRNSTAIQESN-QGAFASPIQLQRRNGSKFSVYD 244

 Qy 233 VDQVKPKIALLKF 245
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 Db 245 VSILIPIALMVY 257

RESULT 2

US-11-263-537-3

; Sequence 3, Application US/11263537
 ; Publication No. US20060100135A1
 ; GENERAL INFORMATION:
 ; APPLICANT: VITETTA, ELLEN S.
 ; APPLICANT: GHETIE, VICTOR F.
 ; APPLICANT: SMALLSHAW, JOAN
 ; APPLICANT: BALUNA, ROXANA G.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
 ; TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
 ; FILE REFERENCE: UTSR:884USC1
 ; CURRENT APPLICATION NUMBER: US/11/263,537
 ; CURRENT FILING DATE: 2005-10-31
 ; PRIOR APPLICATION NUMBER: 10/282,935
 ; PRIOR FILING DATE: 2002-10-29
 ; PRIOR APPLICATION NUMBER: 09/538,873
 ; PRIOR FILING DATE: 2000-03-30
 ; PRIOR APPLICATION NUMBER: 60/126,826
 ; PRIOR FILING DATE: 1999-03-30
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 251
 ; TYPE: PRT
 ; ORGANISM: Abrus precatorius
 US-11-263-537-3

Query Match 24.7%; Score 315; DB 7; Length 251;
 Best Local Similarity 35.3%; Pred. No. 1.4e-20;
 Matches 90; Conservative 39; Mismatches 108; Indels 18; Gaps 8;

Qy 5 VSFSTKGATYITYVNFLNELRVKLKPEGN-SHGIPLLRKKADDP----GKAFVLVALSND 59
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 Db 5 IKFSTEGATSQSYKQFIEALRERLR-GGLIHDIPVL---PDPTTLQERNRYITVELSNS 59

 Qy 60 NGQLAEIAIDVTSVYVVGYQVRNRNSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-G 118
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 Db 60 DTESIEVGIDVTNAYVVAYRAGTQSYFLRDAPSSASDYLFTGTDQHSLPFYGTGDLERW 119

 Qy 119 EKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIR 178
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 Db 120 AHQSRRQQIPLGLQALTHGISFFRGNDN--EEKARTLIVIIQMVAAAARFRYISNRVR 176

 Qy 179 NNFO--QRIRPANNNTISLENKWKGLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQ- 235
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 177 VSIQTGTAFQPDAAMISLENNWDNLSRGVQES-VQDTFPNQVLTNIRNEPVIVDSLHSP 235

 Qy 236 VKPKIALLKFVDKDP 250
 :|:| :| :|
 Db 236 TVAVLALMLFVCNP 250

RESULT 3

US-10-449-902-56587

; Sequence 56587, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56587
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-56587

RESULT 4

US-10-953-349-30545
; Sequence 30545, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30545
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30545

Db	68 PANTGLTLATRADNLYWEGFKSSDGTWWELTPGLIPGATYVG-----FGGTYRD 116
Qy	116 LEGEKAYRETTDLGIEPLRIGIKL---DENAIDNYKPTEIASSLLVVIQMVSSEAARFT 171
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Db	117 LLGDTDKLTNVALGRQQMADAVTALHGRTKADKTSGPKQQAREAVTLLLMVHEATRFQ 176
Qy	172 FIENQIRNNFQQRIRPANNТИSELENWKGLSFQIRTSGANGM--FSEAV--ELERANGK 226
: : : : : : : : : : :	
Db	177 TVSGFVAGLLHPK-----TVEKKSGKISNELKAQ-VNGWQDLSEALLKTDAKPPAGK 227
Qy	227 -----KYYVTAVDQVKPKIALLKFV 246
: : :	
Db	228 PPAKFTPIEKMGVRTAEQAAATLGILLFV 256

RESULT 5

; US-11-056-355B-61236
; Sequence 61236, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 61236
; LENGTH: 277
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(277)
; OTHER INFORMATION: Ceres Seq. ID no. 13661990
US-11-056-355B-61236

US-11-056-355B-61236

Query Match 8.7%; Score 111.5; DB 7; Length 277;
Best Local Similarity 21.9%; Pred. No. 0.02;
Matches 59; Conservative 49; Mismatches 116; Indels 45; Gaps 11;

Qy	59 DNGQLAEIAIDVTSVYVGQVRNRSYFFKD--APDAAYEGLFKNTIKTRLHFGGSYPS 115 : : :: : ::: :
Db	68 PANTGLTLATRADNLYWEGFKSSDGTWELTPGLIPGATYVG-----EGGTYRD 116

Qy 116 LEGEKAYRETTDLGIEPLRIGIKL---DENAIDNYKPTEIASSLLVVVIQMVEAARFT 171
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Ph 117 LCGTDTKLTNTWLGRCGMDAATMUCGDTKADITSGCPKKGCGDNLTTVLMWHTSPE 176

Qy 172 FIENQIRNNFQQRIRPANNNTISLENKGKLSFQIRTSGANGM--FSEAV---ELERANGK 226
: : . : :|| | |||: ::| |||: : : ||

Qy 227 -----KYYTAVDQVKPKIALLKFV 246

DB 228 PPKAKFTPIEKMGVRTAEQAAATLGILLFV 256

US-10-953

; Sequence 30544, Ap

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCONDED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349


```

Db      : : : : ::| | ||:| :: || ||||: : : || 181 TVSGFVAGLLHPK-----TVEKKSGKISNELKAQ-VNGWQDLSEALLKTDAKPPAGK 231
Qy      227 -----KYYVTAVDQVKPKIALLKFV 246
          | | :| : : :| || |
Db      232 PPAKFTPIEKMGVRTAEQAAAATLGILLFV 260

```

RESULT 8

; Sequence 30543, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30543
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30543

RESULT 9

US-11-056-355B-61234
; Sequence 61234, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 61234
; LENGTH: 298
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(298)
; OTHER INFORMATION: Ceres Seq. ID no. 13661988
US-11-056-355B-61234

; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10528
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10528

Query Match 8.5%; Score 108.5; DB 6; Length 232;
Best Local Similarity 23.9%; Pred. No. 0.03;
Matches 60; Conservative 36; Mismatches 94; Indels 61; Gaps 10;

Qy 17 YVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVL-----VALSNDNGQLAEIAIDV 70
Db 7 YLNFVQEAEQDNKKKNKEKDPL---KPKHPVSAFLVYANERRAALREENKSVVEVA--- 60

Qy 71 TSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKAY----- 122
Db 61 ---KITGEEWKNL-----DKKKAPYEVKAKNKETYLQAMEEYKRTKEEEALSQKKEEEE 113

Qy 123 -----RETTDLGIEPLRIGIKKLDENAINDNYKPTEIASSLLVVIQMSEA 167
Db 114 LLKLHKQEALQMLKKKEKTDNLKKEATKKKNEN-VDPNPKKKPASSY----- 162

Qy 168 ARFTFIENQIRNNFQQRIRPANNTIS--LENKGWGLSFQIRT--SGANGMFSEAV--ELE 221
Db 163 --FLFSKDERKKLTTEERPGTNNATVTALISLKWKELSEEKQVYNGKAALKMEAYKKEVE 220

Qy 222 RANGKKYYVTA 232
Db 221 AYNKKSAAATTS 231

RESULT 12
US-10-953-349-10527
; Sequence 10527, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10527
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10527

Query Match 8.5%; Score 108.5; DB 6; Length 245;
Best Local Similarity 23.9%; Pred. No. 0.032;
Matches 60; Conservative 36; Mismatches 94; Indels 61; Gaps 10;

Qy 17 YVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVL-----VALSNDNGQLAEIAIDV 70
Db 20 YLNFVQEAEQDNKKKNKEKDPL---KPKHPVSAFLVYANERRAALREENKSVVEVA--- 73

Qy 71 TSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKAY----- 122
Db 74 ---KITGEEWKNL-----DKKKAPYEVKAKNKETYLQAMEEYKRTKEEEALSQKKEEEE 126

Qy 123 -----RETTDLGIEPLRIGIKKLDENAINDNYKPTEIASSLLVVIQMSEA 167
Db 127 LLKLHKQEALQMLKKKEKTDNLKKEATKKKNEN-VDPNPKKKPASSY----- 175

Qy 168 ARFTFIENQIRNNFQQRIRPANNTIS--LENKGWGLSFQIRT--SGANGMFSEAV--ELE 221

```

Db      || :: : :: || :: : || :: : | : || || ::|| 176 --FLFSKDERKLTEERPGTNNATVTALISLKWKELEEEQVYNGKAALKMEAYKKEVE 233
Qy      222 RANGKKYYVTA 232
Db      || | :|:|| 234 AYNKKSAATTS 244

```

RESULT 13

US-10-953-349-10526
; Sequence 10526, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10526
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10526

Query Match 8.5%; Score 108.5; DB 6; Length 252;
Best Local Similarity 23.9%; Pred. No. 0.033;
Matches 60; Conservative 36; Mismatches 94; Indels 61; Gaps 10;

```

Qy      17 YVNFLNELRVKLKPEGNSHGPILLRKKADDPGKAFV-----VALSNDNGQLAEIAIDV 70
        ||:||:| | :| | :| | | :|:|| :| :| :|:|| 17 YVNFLNELRVKLKPEGNSHGPILLRKKADDPGKAFV-----VALSNDNGQLAEIAIDV 70
Db      27 YLNFVQEAEQDNKKKNKEKDPL---KPKHPVSAFLVYANERRAALREENKSVVEVA--- 80

```

```

Qy      71 TSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKAY----- 122
        :| :| :| | | | :| :| :| :| :| :|:|| 71 TSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKAY----- 122
Db      81 ---KITGEEWKNLS----DKKKAPYEKVAKKNKETYLQAMEEYKRTKEEEALSQKKEEEE 133

```

```

Qy      123 -----RETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLLVVIQMSEA 167
        :| | | | :| :| | :| :| :| :| :| :| 123 -----RETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLLVVIQMSEA 167
Db      134 LLKLHKQEALQMLKKKEKTDLNLIKKEATKKKNEN-VDPNKPKPASSY----- 182

```

```

Qy      168 ARFTFIENQIRNNFQQRIRPANNNTIS--LENKGWKLFSQIRT--SGANGMFSEAV--ELE 221
        || :| :| :| :| | :| :| :| :| :| :| :| 168 ARFTFIENQIRNNFQQRIRPANNNTIS--LENKGWKLFSQIRT--SGANGMFSEAV--ELE 221
Db      183 --FLFSKDERKLTEERPGTNNATVTALISLKWKELEEEQVYNGKAALKMEAYKKEVE 240

```

```

Qy      222 RANGKKYYVTA 232
        || | :|:|| 241 AYNKKSAATTS 251

```

RESULT 14

US-10-471-571A-5500
; Sequence 5500, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 5500
; LENGTH: 876
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(876)
; OTHER INFORMATION: DNA polymerase I
US-10-471-571A-5500

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 101.rup.

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This page gives you Search Results detail for the Application 10717243 and Search Result us-10-717-243-101.rup.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:36:29 ; Search time 257.947 Seconds
(without alignments)
900.105 Million cell updates/sec

Title: US-10-717-243-101
Perfect score: 1277
Sequence: 1 GLDTVSFSTKGATYITYVNF.....AVDQVKPKIALLKFVDKDPK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	%	Match	Length	DB	ID	Description
1	1269	99.4		316	1	RIPG_GELMU		P33186 gelonium mu
2	1235.5	96.8		258	2	Q9S9E4_GELMU		Q9s9e4 gelonium mu
3	398.5	31.2		581	2	Q94BW5_CINCA		Q94bw5 cinnamomum
4	397.5	31.1		580	2	Q94BW3_CINCA		Q94bw3 cinnamomum
5	396.5	31.0		549	2	Q9FV22_CINCA		Q9fv22 cinnamomum
6	391	30.6		299	2	Q8GZN9_9ROSI		Q8gzn9 euphorbia s
7	390.5	30.6		580	2	Q94BW4_CINCA		Q94bw4 cinnamomum
8	365.5	28.6		563	2	Q8GT32_SAMNI		Q8gt32 sambucus ni
9	359.5	28.2		297	2	Q8GZP0_9ROSI		Q8gzp0 euphorbia s
10	356	27.9		563	1	NIGB_SAMNI		P33183 sambucus ni
11	356	27.9		563	2	Q945S2_SAMNI		Q945s2 sambucus ni
12	352.5	27.6		563	2	004367_SAMNI		004367 sambucus ni
13	348	27.3		264	2	Q684J5_MOMCH		Q684j5 momordica c
14	348	27.3		286	1	RIP2_MOMBA		P29339 momordica b
15	348	27.3		286	1	RIP3_MOMCH		P24817 momordica c

16	348	27.3	286	2	Q5PZ05_MOMCH	Q5pz05 momordica c
17	347	27.2	541	2	Q41174_RICCO	Q41174 ricinus com
18	346	27.1	576	1	RICI_RICCO	P02879 ricinus com
19	343.5	26.9	265	1	RIP2_PHYDI	P34967 phytolacca
20	341.5	26.7	294	1	RIP1_TRIAN	P56626 trichosanth
21	341.5	26.7	564	2	Q9AVR2_9DIPS	Q9avr2 sambucus eb
22	337.5	26.4	564	1	AGGL_RICCO	P06750 ricinus com
23	337	26.4	282	1	RIP2_BRYDI	P98184 bryonia dio
24	334.5	26.2	527	1	ABRB_ABRPR	Q06077 abrus preca
25	332.5	26.0	294	1	RIPA_PHYAM	Q03464 phytolacca
26	330.5	25.9	293	2	Q8VYU0_9ROSI	Q8vyu0 jatropha cu
27	330	25.8	252	2	Q38760_ABRPR	Q38760 abrus preca
28	329.5	25.8	294	2	Q8H1W1_PHYAM	Q8h1w1 phytolacca
29	328.5	25.7	275	2	Q84LJ1_GYNPE	Q84lj1 gynostemma
30	327.5	25.6	277	2	Q84JR1_GYNPE	Q84jr1 gynostemma
31	327	25.6	313	1	RIP1_PHYAM	P10297 phytolacca
32	327	25.6	313	2	Q53YN2_PHYAM	Q53yn2 phytolacca
33	327	25.6	313	2	Q6PWU4_PHYAM	Q6pwu4 phytolacca
34	326.5	25.6	277	2	Q8GV09_GYNPE	Q8gv09 gynostemma
35	326	25.5	289	2	Q41216_TRIKI	Q41216 trichosanth
36	325.5	25.5	275	2	Q8H1Y4_GYNPE	Q8h1y4 gynostemma
37	325.5	25.5	293	2	Q8S452_9ROSI	Q8s452 jatropha cu
38	325.5	25.5	298	2	Q5FOI3_GYNPE	Q5foi3 gynostemma
39	325	25.5	567	2	Q6H267_VISAL	Q6h267 viscum albu
40	323.5	25.3	277	2	Q8GV11_GYNPE	Q8gv11 gynostemma
41	323	25.3	289	1	RIPT_TRIKI	P09989 trichosanth
42	323	25.3	289	2	Q94KE4_TRIKI	Q94ke4 trichosanth
43	322	25.2	289	2	Q84SV8_TRIKI	Q84sv8 trichosanth
44	321.5	25.2	565	2	004071_SAMNI	004071 sambucus ni
45	321	25.1	251	2	Q7DM12_ABRPR	Q7dm12 abrus preca

ALIGNMENTS

RESULT 1
RIPG_GELMU

ID RIPG_GELMU STANDARD; PRT; 316 AA.
AC P33186;
DT 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 2.
DT 07-FEB-2006, entry version 44.
DE Ribosome-inactivating protein gelonin precursor (EC 3.2.2.22) (rRNA N-glycosidase).
DE Name=GEL;
OS Gelonium multiflorum (Euphorbiaceae himalaya).
OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
OC Gelonieae; Gelonium.
NCBI_TaxID=3979;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RX MEDLINE=94085781; PubMed=7916721; DOI=10.1016/0378-1119(93)90097-M;
RA Nolan P.A., Garrison D.A., Better M.;
RT "Cloning and expression of a gene encoding gelonin, a ribosome-inactivating protein from *Gelonium multiflorum*.";
RL Gene 134:223-227(1993).
RN [2]
RP PROTEIN SEQUENCE OF 47-93.
RC TISSUE=Seed;
RX MEDLINE=89326691; PubMed=2753596;
RA Montecucchi P.-C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
RA Lappi D.;
RT "N-terminal sequence of some ribosome-inactivating proteins.";
RL Int. J. Pept. Protein Res. 33:263-267(1989).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE=95333189; PubMed=7608981;
RA Hosur M.V., Nair B., Satyamurthy P., Misquith S., Surolia A.,
RA Kannan K.K.;
RT "X-ray structure of gelonin at 1.8-A resolution.";
RL J. Mol. Biol. 250:368-380(1995).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC -!- SUBUNIT: Homodimer.

CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RIP subfamily.
 CC
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 CC
 DR EMBL; L12243; AAA16312.1; -; mRNA.
 DR PIR; JT0753; JT0753.
 DR HSSP; P09989; 1MRJ.
 DR InterPro; IPRO001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;
 KW Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 26 Potential.
 FT PROPEP 27 46
 FT PROPEP 27 46 /FTId=PRO_0000030786.
 FT CHAIN 47 297 Ribosome-inactivating protein gelonin.
 FT PROPEP 298 316 /FTId=PRO_0000030787.
 FT PROPEP 298 316 Removed in mature form.
 FT ACT_SITE 212 212 /FTId=PRO_0000030788.
 FT CARBOHYD 235 235 N-linked (GlcNAc. .).
 FT DISULFID 90 96
 FT CONFLICT 90 90 C -> K (in Ref. 2).
 FT CONFLICT 93 93 P -> D (in Ref. 2).
 SQ SEQUENCE 316 AA; 35419 MW; 1252F3E710901B85 CRC64;

Query Match 99.4%; Score 1269; DB 1; Length 316;
 Best Local Similarity 99.2%; Pred. No. 2.8e-98;
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db	47 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKCFVLVALSNDN 106
Qy	61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
Db	107 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 166
Qy	121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180
Db	167 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 226
Qy	181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db	227 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 286
Qy	241 ALLKFVDKDPK 251
Db	287 ALLKFVDKDPK 297

RESULT 2
 Q9S9E4_GELMU
 ID Q9S9E4_GELMU PRELIMINARY; PRT; 258 AA.
 AC Q9S9E4;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 21.
 DE rRNA -glycosidase (EC 3.2.2.22) (rRNA N-glycosidase).
 OS Gelonium multiflorum (Euphorbiaceae himalaya).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
 OC Gelonieae; Gelonium.
 OX NCBI_TaxID=3979;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=96006751; PubMed=7553224;
 RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,
 RA Toman P.D., Cheung L.;
 RT "Amino acid sequence analysis, gene construction, cloning, and
 RT expression of gelonin, a toxin derived from *Gelonium multiflorum*.";
 RL J. Interferon Cytokine Res. 15:547-555(1995).

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CC
DR HSSP; P09989; 1MRJ.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
SQ SEQUENCE 258 AA; 28826 MW; 13D68E673F4D6B06 CRC64;

Query Match 96.8%; Score 1235.5; DB 2; Length 258;
Best Local Similarity 95.4%; Pred. No. 1.4e-95;
Matches 247; Conservative 1; Mismatches 2; Indels 9; Gaps 2;

Qy	1	GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNNSHGIPLLRKKADDPGKAFVLVALSDND	60
Db	1	GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNNSHGIPLLR-KGDDPGKCFVLVALSDND	59
Qy	61	GQLAEIAIDVTSVYVGQVRNRSYFFKDAPDAAYEGLFKNTI-----KTRLHFEGGS	112
Db	60	GQLAEIAIDVTSVYVGQVRNRSYFFKDAPDAAYEGLFKNTIKNPLLFGGKTRLHFEGGS	119
Qy	113	YPSLEGEKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMSEAARFTF	172
Db	120	YPSLEGEKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMSEAARFTF	179
Qy	173	IENQIRNNFQQIRPANNTISLENKGWLKFQIRTSANGMFSEAVELERANGKYYVTA	232
Db	180	IENQIRNNFQQIRPANNTISLENKGWLKFQIRTSANGMFSEAVELERANGKYYVTA	239
Qy	233	VDQVKPKIALLKFVDKDPK	251
Db	240	VDQVKPKIALLKFVDKDPE	258

RESULT 3

Q94BW5_CINCA
ID Q94BW5_CINCA PRELIMINARY; PRT; 581 AA.
AC Q94BW5;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Type 2 ribosome-inactivating protein cinnamomin I precursor.
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated
from the seeds of camphor tree and their expression patterns.";
RL Gene 284:215-223(2002).

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DR EMBL; AY039801; AAK82458.1; -; Genomic_DNA.
DR HSSP; P02879; '2AAI.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PRO0396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.

DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 KW Signal.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 581 type 2 ribosome-inactivating protein
 cinnamomin I.
 SQ SEQUENCE 581 AA; 64216 MW; 6E8F5FB8FBA3D196 CRC64;

 Query Match 31.2%; Score 398.5; DB 2; Length 581;
 Best Local Similarity 39.7%; Pred. No. 1.2e-24;
 Matches 100; Conservative 46; Mismatches 93; Indels 13; Gaps 8;

 Qy 4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDP-GKAFVLVALSN---D 59
 ||:|:|| || :| :|| :||:|:::| | | |:|| ||| |
 Db 35 TVTFTTKNATKTSYTFQIEALRAQLASGEYPHGPVMRERSTVPDSKRFILVELSNWAAD 94

 Qy 60 NGQLAEIAIDVTSVYVVGYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSEG 118
 :|:|:||:| ||| :| :||:| :| ||| | | :| :| | ||| |||
 Db 95 SP--VTLAVDVTNAYVAYRTGSQFFLREDNPDPAIENLLPDTKRYTFPFSGSYTDLEG 152

 Qy 119 EKA-YRETTDLGIEPLRIGIKKKLDENAIKDNYKPTEIASSLLVVIQMVAARFTFIENQI 177
 || | |:|| | | | :| ::| :| ||:|||||:|| | | | | |:
 Db 153 VAGERREEILLGMDPLENAISALWISNLNQQR--ALARSLIVVIQMVAEAVRFRFIEYRV 210

 Qy 178 RNNFQ--QRIRPANNTISLENKGWLKFQIRTSANGMFSEAVELERANGKKYYTAV-D 234
 | :| :| || :| ||| | | :| | | | | | :| | | | |:
 Db 211 RGSISRAEMFRPDPAMLSLENKWSALSNAVQQSNQGGVFSSPVELRSISNKPVYGVSD 270

 Qy 235 QVKPKIALLKTV 246
 :| :|::|:
 Db 271 RVISGLAIMLF 282

RESULT 4
 Q94BW3_CINCA
 ID Q94BW3_CINCA PRELIMINARY; PRT; 580 AA.
 AC Q94BW3;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Type 2 ribosome-inactivating protein cinnamomin III precursor.
 OS Cinnamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
 OC Cinnamomum.
 OX NCBI_TaxID=13429;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=2188636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
 RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
 RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated
 from the seeds of camphor tree and their expression patterns.";
 RL Gene 284:215-223(2002).
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 DR EMBL; AY039803; AAK82460.1; -; Genomic_DNA.
 DR HSSP; P02879; 2AAI.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 2.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 KW Signal.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 580 type 2 ribosome-inactivating protein
 cinnamomin III.
 SQ SEQUENCE 580 AA; 64422 MW; 940D10F01E7FB558 CRC64;

 Query Match 31.1%; Score 397.5; DB 2; Length 580;
 Best Local Similarity 39.8%; Pred. No. 1.5e-24;
 Matches 101; Conservative 47; Mismatches 89; Indels 17; Gaps 9;

Qy 4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDP-GKAFVLVALSN---D 59
 ||:||:|| | :| :|| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
 Db 35 TVTFTTKNATKTSYTQFIEALRAQLASGEEPHGIPVMRERSTVPDFSKRFILVELSNWAAD 94

 Qy 60 NGQLAEIAIDVTSVYVVGYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFVGSYPSLE- 117
 : :||:||: || | : ::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
 Db 95 SP--VTLAVDVTNAYVAVRTGSQSSFLREDNPDAIENLLPDTKRYTFPFSGSYTDLER 152

 Qy 118 --GEKAYRETTDLGIEPLRIGIKLDEAIDNYKPTEIASSLLVVIQMVAEAVRFRFIEEN 175
 ||:|| | ||:|| | | : : : :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
 Db 153 VAGER--REEILLGMDPLENAISALWISNLNQQR--ALARSLIVVIQMVAEAVRFRFIEY 208

 Qy 176 QIRNNF--QQRIRPANTTISLENKGWLKFQIRTSGANGMFSEAVELERANGKKYYVTAV 233
 ::|| : :|| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
 Db 209 RVRESITRAEMFRPDPAMLSLENKWSALSNAVQQSNQGGVFSSPVELRSISNKPVYVGSV 268

 Qy 234 -DQVKPKIALLKFX 246
 :|| :||:||:
 Db 269 SDRVISGLAIMLFI 282

RESULT 5

Q9FV22_CINCA
 ID Q9FV22_CINCA PRELIMINARY; PRT; 549 AA.
 AC Q9FV22;
 DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2001, sequence version 1.
 DT 07-FEB-2006, entry version 19.
 DE Type II ribosome-inactivating protein cinnamomin (Fragment).
 OS Cinnamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
 OC Cinnamomum.
 OX NCBI_TaxID=13429;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Xie L., Liu W.-Y., Wang E.-D.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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 DR EMBL; AF259548; AAF68978.2; -; mRNA.
 DR HSSP; P02879; 2AAI.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; GO:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPRO000772; Ricin_B_lectin.
 DR InterPro; IPRO001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 2.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 FT NON_TER 1 1
 SQ SEQUENCE 549 AA; 60649 MW; 02607FE607CA44B0 CRC64;

Query Match 31.0%; Score 396.5; DB 2; Length 549;
 Best Local Similarity 39.7%; Pred. No. 1.7e-24;
 Matches 100; Conservative 46; Mismatches 93; Indels 13; Gaps 8;

 Qy 4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDP-GKAFVLVALSN---D 59
 ||:||:|| | :| :|| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
 Db 3 TVTFTTKNATKTSYTQFIEALRAQLASGEEPHGIPVMRERSTVPDFSKRFILVELSNWAAD 62

 Qy 60 NGQLAEIAIDVTSVYVVGYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFVGSYPSLEG 118
 : :||:||: || | : ::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
 Db 63 SP--VTLAVDVTNAYVAVRTGSQSSFLREDNPDAIENLLPDTKRYTFPFSGSYTDLEG 120

 Qy 119 EKA-YRETTDLGIEPLRIGIKLDEAIDNYKPTEIASSLLVVIQMVAEAVRFRFIEENQI 177
 || | ||:|| | | : : : :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
 Db 121 VAGERREEILLGMDPLENAISALWISNLNQQR--ALARSLIVVIQMVAEAVRFRFIEYRV 178

 Qy 178 RNNFQ--QQRIRPANTTISLENKGWLKFQIRTSGANGMFSEAVELERANGKKYYVTAV-D 234
 | : : || :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
 Db 179 RGSISRAEMFRPDPAMLSLENKWSALSNAVQQSNQGGVFSSPVELRSISNKPVYVGVS 238

Qy 235 QVKPKIAALLKFV 246
 :| :|: :|:
 Db 239 RVISGLAIMALFI 250

RESULT 7

Q94BW4_CINCA
ID Q94BW4_CINCA PRELIMINARY; PRT; 580 AA.
AC Q94BW4;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Type 2 ribosome-inactivating protein cinnamomin II precursor.
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated
from the seeds of camphor tree and their expression patterns.";
RL Gene 284:215-223(2002).
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DR EMBL; AY039802; AAK82459.1; -; Genomic_DNA.
DR HSSP; P02879; 2AAI.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
KW Signal.
FT SIGNAL 1 32 Potential.
FT CHAIN 33 580 type 2 ribosome-inactivating protein
FT cinnamomin II.
SQ SEQUENCE 580 AA; 64266 MW; 37E4289ECCE0CBFF CRC64;

Query Match 30.6%; Score 390.5; DB 2; Length 580;
Best Local Similarity 39.8%; Pred. No. 5.8e-24;
Matches 101; Conservative 44; Mismatches 92; Indels 17; Gaps 9;

Qy 4 TVSFSTKGATYITYVNFLNELRVKLPKPEGNSHGIPLLRKKADDP-GKAFVLVALSN---D 59
Db ||::|:|| || :| :|| :|| :||:||:|| :| | | :|| || || |
Qy 35. TVTFTTKNATKTTSYTQFIEALRAQLASGEYPHGIPVMDGSTVPDSKRFLVLSNWAAD 94

Qy 60 NGQLAEIAIDVTSVYVGYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSE- 117
Db :||:||:|| | : ::||:| :| || || | :| :| || || ||
Qy 95 SP--VALAVDVTNAYVVAYRTGSQSFFLREDNPDPAIENLLPDTKRYTFPFSGSYTDLER 152

Qy 118 --GEKAYRETTDLGIEPLRIGIKKLDENAINDKPTEIASSLLVVIQMVAEAVRFRFIEY 175
Db || | | ||:|| | | :|| :| :||:|||||:|| || |||
Qy 153 VAGE--LREEILLGMDPLENAISALWTSNLNQQR--ALARSLIVVIQMVAEAVRFRFIEY 208

Qy 176 QIRNNF--QQRIRPANNNTISLENWKGLSFQIRTSANGMFSEAVELERANGKYYVTAV 233
Db ::|| :| :|| :||||| || ::| | :|| || | :| || :|
Qy 209 RVRESITRAEMFRPDPAMLSENKWSALSNAVQQSNQGGVFSSPVELRSISNKPVYVGSV 268

Qy 234 -DQVKPKIALLKFV 246
Db ||:| :||:|:
Qy 269 SDRVVISGLAIMLFI 282

RESULT 8
Q8GT32_SAMNI
ID Q8GT32_SAMNI PRELIMINARY; PRT; 563 AA.
AC Q8GT32;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Type 2 ribosome-inactivating protein Nigrin 1 (EC 3.2.2.22).
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;

OC asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Girbes T., Arias F.J., Antolin P.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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DR EMBL; AF249280; AAN86130.1; -; mRNA.
DR HSSP; Q9AVR2; 1HWM.
DR SMR; Q8GT32; 26-274, 299-560.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 563 AA; 62173 MW; OEB236421FC5E04F CRC64;

Query Match 28.6%; Score 365.5; DB 2; Length 563;
Best Local Similarity 41.0%; Pred. No. 7.1e-22;
Matches 94; Conservative 38; Mismatches 80; Indels 17; Gaps 8;

Qy 1 GLD--TVSFSTKGATYITYVNFLNELRVKLKPEG--NSHGIPLLRKKADDPGKA-FVLVA 55
|:| :||: || || :||: || | :||:||:::| :| :|||
Db 25 GIDYPSVSFNLDGAKSATYRDFLSNLR-KTVATGYEVNGLPVLRRESEVQVKSRFVLVP 83

Qy 56 LSNDNGQLAEIAIDVTSVYVVGYQVRNRNSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPS 115
|:| || :||:||:|| :| ||||||| : || | : || |:|| :|
Db 84 LTNYNGNTVTLAVDVTNLYVVAFSGNANSYFFKDATEVQKSNLFVGTKQNTLSFTGNYDN 143

Qy 116 LE-GEKAYRETTDLGIEPLRIGIKKKDENADNYKPTEIASSLLVVIQMVSEAARFTFIE 174
|| ||:|| || | | | | :| ||||||||||||| :||
Db 144 LETAAANTRRESIELGPSPLDGAITS-----YHGDSVARSLVVIQMVSEAARFRYIE 196

Qy 175 NQIRNNFQQ--RIRPANNNTISLENKWKLSFQIRTSGAN-GMFSEAVEL 220
::| :|| | : :||:|| | :|| :| | || |:||
Db 197 QEVRRSLQQATSFTPNAASMLSMENNWSMSLEIQQAGNNVSPFSGTVQL 245

RESULT 9
Q8GZP0_9ROSI
ID Q8GZP0_9ROSI PRELIMINARY; PRT; 297 AA.
AC Q8GZP0;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Ribosome inactivating protein Euserratin 1 precursor (EC 3.2.2.22).
GN Name=Eus1;
OS Euphorbia serrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Euphorbioideae;
OC Euphorbieae; Euphorbia.
OX NCBI_TaxID=196589;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Girbes T., Arias F.J., Benvenuto E.;
RT "Purification, characterization and molecular cloning of euserratins,
RT new type 1 ribosome-inactivating proteins from Euphorbia serrata L.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; AF457874; AAO15530.1; -; mRNA.

DR HSSP; P33185; 1BRY.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor;
 KW Signal; Toxin.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 297 ribosome inactivating protein Euserratin
 FT 1.
 SQ SEQUENCE 297 AA; 33146 MW; A5269E1DDB91287A CRC64;

 Query Match 28.2%; Score 359.5; DB 2; Length 297;
 Best Local Similarity 39.8%; Pred. No. 9.9e-22;
 Matches 98; Conservative 40; Mismatches 97; Indels 11; Gaps 7;

 Qy 4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKAD--DPGKAFLVALSN-DN 60
 || ||:| :| :| ::||| |: :|| ||||||| :|| | | :||| :|||
 Db 29 TVKFTTHLASVGSYQTLM SALRVNLESKLESHNIPLLRKPS DITDQN K-YLLVELTNYDT 87

 Qy 61 GQLAELIAIDVTSVYVVGYQVRNRNSYFFKDAPDAAYEGLFKNTIKTRLHF GG SYP SLEGEK 120
 : :||| :| :|||:||| :||| :||| | ||| :| :||| :| :|||
 Db 88 KRTVTLALT VLN VYVIG YKSGT KSF FLKDAPS DAK TLLFT DTT PKT LEV DT NYNNL-GD- 145

 Qy 121 AYRETTDLGIEPLRIGIKKL DENAIDNYK-PTEIASSL VVIQM VSE AARFTFIENQIRN 179
 | ||| :| | | | | | :| :||| :||| :||| :||| :| :|||
 Db 146 --RSKVGLGIPALKNA INIL--NQFDGVSTDQDFKHSLLIVIQM VSE AARFKF IQLKIEG 201

 Qy 180 NFQQRIRP ANNTISLENK W GKLSF QIRT SGANGMF SEAVE LERANGK YYVTA DVQVKPK 239
 :| :||| :| | | | | :| :||| :||| :| :||| :| :|||
 Db 202 GLLTQYLPK PDT ISYQNNWSALSKSIQLADANGRLSE SVT LKYEDGKDRVVF MV EQVQRD 261

 Qy 240 I ALLKF 245
 :| :||| :
 Db 262 ISLLLY 267

RESULT 10
NIGB_SAMNI
ID NIGB_SAMNI STANDARD; PRT; 563 AA.
AC P33183; P33184; P93542;
DT 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.
DT 05-DEC-2001, sequence version 2.
DT 07-FEB-2006, entry version 56.
DE Nigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chain
DE (EC 3.2.2.22) (rRNA N-glycosidase); Nigrin b B chain].
OS Sambucus nigra (European elder).
OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Bark;
RX MEDLINE=96215449; PubMed=8647092;
RA Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
RT "Characterization and molecular cloning of Sambucus nigra agglutinin V
RT (nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein
RT from the bark of elderberry (Sambucus nigra).";
RL Eur. J. Biochem. 237:505-513(1996).
RN [2]
RP PROTEIN SEQUENCE OF 26-49 AND 298-321.
RC TISSUE=Bark;
RX MEDLINE=94003077; PubMed=8400135;
RA Girbes T., Cidores L., Ferreras J.M., Rojo M.A., Iglesias R.,
RA Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;
RT "Isolation and partial characterization of nigrin b, a non-toxic novel
RT type 2 ribosome-inactivating protein from the bark of Sambucus nigra
RT L.";
RL Plant Mol. Biol. 22:1181-1186(1993).

CC -!- FUNCTION: Non-toxic type 2 RIP which strongly inhibits mammalian protein synthesis but does not affect plant nor bacterial protein synthesis. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal subunits by removing adenine from position 4,324 of 28S rRNA.
 CC -!- FUNCTION: The B chain is a galactose-specific lectin that facilitates the binding of nigrin b to the cell membrane that precedes endocytosis.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SUBUNIT: Disulfide-linked dimer of A and B chains.
 CC -!- SIMILARITY: In the N-terminal section; belongs to the ribosome-inactivating protein family. Type 2 RIP subfamily.
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC

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DR EMBL; U41299; AAB39475.1; -; mRNA.
 DR PIR; S37382; S37382.
 DR PIR; S37383; S37383.
 DR HSSP; Q9AVR2; 1HWM.
 DR SMR; P33183; 26-274, 299-560.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 2.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_BLECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Direct protein sequencing; Glycoprotein; Hydrolase; Lectin;
 KW Plant defense; Protein synthesis inhibitor; Repeat; Signal; Toxin.
 FT SIGNAL 1 25
 FT CHAIN 26 297 Nigrin b A chain.
 FT /FTId=PRO_0000030744.
 FT CHAIN 298 563 Nigrin b B chain.
 FT /FTId=PRO_0000030745.
 FT DOMAIN 305 431 Ricin B-type lectin 1.
 FT REPEAT 316 356 1-alpha.
 FT REPEAT 357 397 1-beta.
 FT REPEAT 400 432 1-gamma.
 FT DOMAIN 434 559 Ricin B-type lectin 2.
 FT REPEAT 445 482 2-alpha.
 FT REPEAT 486 524 2-beta.
 FT REPEAT 527 554 2-gamma.
 FT ACT_SITE 188 188 By similarity.
 FT CARBOHYD 221 221 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 368 368 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 376 376 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 483 483 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 537 537 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 274 302 Interchain (between B and A chains) (By similarity).
 FT DISULFID 319 338 By similarity.
 FT DISULFID 360 377 By similarity.
 FT DISULFID 448 463 By similarity.
 FT DISULFID 489 506 By similarity.
 FT CONFLICT 39 39 K -> V (in Ref. 2).
 SQ SEQUENCE 563 AA; 62300 MW; F250CBE24621BF14 CRC64;

Query Match 27.9%; Score 356; DB 1; Length 563;
 Best Local Similarity 41.1%; Pred. No. 4.5e-21;
 Matches 90; Conservative 36; Mismatches 77; Indels 16; Gaps 7;

Qy 1 GLD--TWSFSTKGATYITYVNFLNELRVKLPEG--NSHGIPLLRKKADDPGKA-FVLVA 55
 ||: :||: || || :||: || | :||:||:||::: |: ||||
 Db 25 GIDYPSVSFNLDGAKSATYRDFLSNLR-KTVATGTYEVNGLPVLRRESEVQVKSRFVLVP 83

Qy 56 LSNDNGQLAIEIAIDVTSTVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPS 115
 ||: || :||:||:||: || || || : || | : || ||:|| :||:
 Db 84 LTNYNGNTVTLAVDVTNLYVVAFSGNANSYFFKDATEVQKSNLFGTKQNTLSFTGNYDN 143

Qy 116 LE-GEKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVEAARFTFIE 174
 || ||: :|| || | | | :| ||||||||||| :||:
 Db 144 LETAANTRRESIELGPSPLDGAITS-----YHGDSVARSLIVVIQMVEAARFRYIE 196

Qy 175 NQIRNNFQQ--RIRPANNNTISLENKWGKLSFQIRTSGAN 211
::| :|| | :||| | :| :|: :| |
Db 197 QEVRRSLQQATSFTPNALMLSMENNWSSMSLEIQQAGNN 235

RESULT 11
Q945S2_SAMNI
ID Q945S2_SAMNI PRELIMINARY; PRT; 563 AA.
AC Q945S2;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Ribosome-inactivating protein.
GN Name=Avl;
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Van Damme E.J.M.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF409135; AAL04123.1; -; mRNA.
DR HSSP; Q9AVR2; 1HWM.
DR SMR; Q945S2; 26-274, 299-560.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
SQ SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;

Query Match 27.9%; Score 356; DB 2; Length 563;
Best Local Similarity 41.1%; Pred. No. 4.5e-21;
Matches 90; Conservative 36; Mismatches 77; Indels 16; Gaps 7;

Qy 1 GLD--TWSFSTKGATYITYVNFLNELRVKLKPEG--NSHGIPLLRKKADDPGKA-FVLVA 55
|:| :||: || || :||: || | :||:||:||: |: |||||
Db 25 GIDYPSVSFNLDGAKSATYRDFLSNLR-KTVATGTYEVNGLPVLRSEEVQVKSRFVLVP 83

Qy 56 LSNDNGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPS 115
|:| || :||:||:|| : | ||||| : || | | : | | :| :
Db 84 LTNYNGNTVTLAVDVTNLYVVAFSGNANSYFFKDATEVQKSNLFGTKQNTLSFTGNYDN 143

Qy 116 LE-GEKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLIVVIQMVEARFTFIE 174
|| | :||:|| | | | | | :| | ||| | | | | | :||
Db 144 LETAANTRRESIELGPSPLDGAISSL-----YHGDSVARSLIVVIQMVEARFRYIE 196

Qy 175 NQIRNNFQQ--RIRPANNNTISLENKWGKLSFQIRTSGAN 211
::| :|| | :||| | :| :|: :| |
Db 197 QEVRRSLQQATSFTPNALMLSMENNWSSMSLEIQQAGNN 235

RESULT 12
O04367_SAMNI
ID O04367_SAMNI PRELIMINARY; PRT; 563 AA.
AC O04367;
DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT 01-JUL-1997, sequence version 1.
DT 07-FEB-2006, entry version 33.
DE Ribosome inactivating protein precursor.
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
 OX NCBI_TaxID=4202;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98112023; PubMed=9450339;
 RA Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
 RA Peumans W.J.;
 RT "The major elderberry (*Sambucus nigra*) fruit protein is a lectin
 derived from a truncated type 2 ribosome-inactivating protein.";
 RL Plant J. 12:1251-1260(1997).
 CC
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 CC
 DR EMBL; U76524; AAC15886.1; -; mRNA.
 DR HSSP; Q9AVR2; 1HWM.
 DR SMR; 004367; 26-276, 299-560.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 2.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Signal.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 297 ribosome inactivating protein, A chain.
 FT CHAIN 298 563 ribosome inactivating protein, B chain.
 SQ SEQUENCE 563 AA; 62337 MW; 3ED2B6C08E796205 CRC64;
 Query Match 27.6%; Score 352.5; DB 2; Length 563;
 Best Local Similarity 39.7%; Pred. No. 8.9e-21;
 Matches 91; Conservative 37; Mismatches 86; Indels 15; Gaps 7;
 Qy 1 GLD--TVSFSTKGATYITYVNFLNELR--VVLKPEGNSHGIPLLRKKADDPGK-AFVLVAL 56
 Db 25 GIDYPSVSFNLAGAKSATYRDFLKNLRTIVATGTYEVNGLPVLRRESEVQVKNRFLVLL 84
 Qy 57 SNDNGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSL 116
 Db 85 TNYNGNTVTLAVDVTNLVYVAFSANANSYFFKDATQLQKSNLFVGTRQHTLPFTGNYDNL 144
 Qy 117 E-GEKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVIQMVEAARFTFIEN 175
 Db 145 ETAAGTRRESIELGPSPLDGAITS-----YYDESVARSLLVIQMVEAARFRYIEQ 197
 Qy 176 QIRNNFQQR--IRPANNTISLENKGWKLFSQIRTSGAN-GMFSEAVELE 221
 Db 198 EVRRSLQQTAGFTPNALMSMENNWSMSLEVQQSGDNVSPFTGTVQLQ 246

RESULT 13
 Q684J5_MOMCH
 ID Q684J5_MOMCH PRELIMINARY; PRT; 264 AA.
 AC Q684J5;
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Type I ribosome inactivating protein precursor (Fragment).
 GN Name=rip;
 OS Momordica charantia (Bitter gourd) (Balsam pear).
 OC Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
 OX NCBI_TaxID=3673;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HN1;
 RA Nguyen Dinh C., Nguyen Thuy D., Le Thi Thu H., Nguyen Huy H.,
 RA Tran Thi Phuong L., Nong Van H.;
 RT "Expression of a gene encoding ribosome inactivating protein from
 bitter melon (*Momordica charantia*).";
 RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

RESULT 14
RIP2_MOMBA
ID RIP2_MOMBA STANDARD; PRT; 286 AA.
AC P29339;
DT 01-DEC-1992, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-1992, sequence version 1.
DT 07-FEB-2006, entry version 40.
DE Ribosome-inactivating protein momordin II precursor (EC 3.2.2.22)
DE (rRNA N-glycosidase).
OS Momordica balsamina (Bitter gourd) (Balsam apple).
OC Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
OX NCBI_TaxID=3672;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Seed;
RX MEDLINE=93027170; PubMed=1408771;
RA Ortigao M., Better M.;
RT "Momordin II, a ribosome inactivating protein from Momordica
RT balsamina, is homologous to other plant proteins.";
RL Nucleic Acids Res. 20:4662-4662(1992).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at o
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.

CC Type 1 RIP subfamily.
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 CC
 DR EMBL; Z12175; CAA78166.1; -; Genomic_DNA.
 DR PIR; S25560; S25560.
 DR SMR; P29339; 24-286.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 23
 FT CHAIN 24 286 Ribosome-inactivating protein momordin
 II.
 FT /FTId=PRO_0000030772.
 FT ACT_SITE 181 181 By similarity.
 SQ SEQUENCE 286 AA; 32032 MW; 3B89FF1AE6B25986 CRC64;
 Query Match 27.3%; Score 348; DB 1; Length 286;
 Best Local Similarity 37.4%; Pred. No. 8.7e-21;
 Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;
 Qy 5 VSFSTKGATYITYVNFLNELRVKKPENSHGIPLLRKKADDPGKAFVLVALSNDNGQLA 64
 Db 25 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISD-SRRFILLDTSYAYETI 83
 Qy 65 EIAIDVTSVVVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSE-GEKAYR 123
 Db 84 SVAIDVTNVVYVAYRTRDVSYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAHKIR 143
 Qy 124 ETTDLGIEPLRIGIKKLDENADNYKPTEIASSLTVVIQMSEAARFTFIENQIRNNFQQ 183
 Db 144 ENIDLGLPALSSAI----TTLFYNAQSAPSALLVLIQTTAEARFKYIERHVAKYVAT 198
 Qy 184 RIRPANNITISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYVTAVDQ--VKPKI 240
 Db 199 NFKPNLAIISLENOQSALSQIFLAQNQGGKFRNPVDLIKPTGERFQVTNVDSVVKGNI 258
 Qy 241 ALL 243
 Db 259 KLL 261

RESULT 15
 RIP3_MOMCH
 ID RIP3_MOMCH STANDARD; PRT; 286 AA.
 AC P24817; Q41257; Q9FSH2; Q9FUV7;
 DT 01-MAR-1992, integrated into UniProtKB/Swiss-Prot.
 DT 26-APR-2004, sequence version 2.
 DT 07-FEB-2006, entry version 46.
 DE Ribosome-inactivating protein beta-momorcharin precursor (EC 3.2.2.22)
 DE (rRNA N-glycosidase) (MAP30) (B-MMC).
 GN Name=MAP30; Synonyms=RIP;
 OS Momordica charantia (Bitter gourd) (Balsam pear).
 OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytina; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
 OX NCBI_TaxID=3673;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Leaf;
 RX MEDLINE=95394347; PubMed=7665070; DOI=10.1016/0378-1119(95)00186-A;
 RA Lee-Huang S., Huang P.L., Chen H.-C., Huang P.L., Bourinbaiar A.,
 RA Huang H.I., Kung H.-F.;
 RT "Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter
 melon.";
 RL Gene 161:151-156(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Quanhong Y., Rihe P., Aisheng X.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 23-286.
 RA Wei Y.-F., Cai L.-B., Zhuang W.;

RT "Cloning rip gene and identification of its resistance to Aspergillus
 RT flavus.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 23-286.
 RA Nguyen Huy H., Nghiem Ngoc M., Dao Huy P., Le Tran B., Nong Van H.;
 RT "Expression of a RIP gene from Momordica charantia in E. coli.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP PROTEIN SEQUENCE OF 24-67.
 RC TISSUE=Seed;
 RX MEDLINE=91032105; PubMed=1699801; DOI=10.1016/0014-5793(90)80438-O;
 RA Lee-Huang S., Huang P.L., Nara P.L., Chen H.-C., Kung H.-F., Huang P.,
 RA Huang H.I., Huang P.L.;
 RT "MAP 30: a new inhibitor of HIV-1 infection and replication.";
 RL FEBS Lett. 272:12-18(1990).
 RN [6]
 RP STRUCTURE BY NMR OF 24-286, AND DNA-BINDING.
 RX PubMed=10571185; DOI=10.1016/S0092-8674(00)81529-9;
 RA Wang Y.-X., Neamati N., Jacob J., Palmer I., Stahl S.J., Kaufman J.D.,
 RA Huang P.L., Huang P.L., Winslow H.E., Pommier Y., Wingfield P.T.,
 RA Lee-Huang S., Bax A., Torchia D.A.;
 RT "Solution structure of anti-HIV-1 and anti-tumor protein MAP30:
 RT structural insights into its multiple functions.";
 RL Cell 99:433-442(1999).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 24-272.
 RX PubMed=10329776; DOI=10.1107/S0907444999003297;
 RA Yuan Y.-R., He Y.-N., Xiong J.-P., Xia Z.-X.;
 RT "Three-dimensional structure of beta-momorcharin at 2.55 Å
 RT resolution.";
 RL Acta Crystallogr. D 55:1144-1151(1999).
 CC -!- FUNCTION: Irreversibly relaxes supercoiled DNA and catalyzes
 CC double-stranded breakage. Acts also as a ribosome inactivating
 CC protein.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- PTM: Bound to a branched hexasaccharide.
 CC -!- MISCELLANEOUS: Possesses anti-HIV and antitumoral activities.
 CC Inhibits HIV-1 integrase.
 CC -!- MISCELLANEOUS: Manganese or zinc required for enhancing substrate
 CC binding rather than catalysis.
 CC -!- MISCELLANEOUS: The oligosaccharide does not influence the fold of
 CC the polypeptide chain and probably does not play a role in the
 CC enzymatic function.
 CC -!- MISCELLANEOUS: Is not toxic to uninfected normal cells as it
 CC cannot enter into them.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RIP subfamily.
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 CC -----
 DR EMBL; S79450; AAB35194.2; -; Genomic_DNA.
 DR EMBL; AF284811; AAG33028.1; -; Genomic_DNA.
 DR EMBL; AY523412; AAS17014.1; -; mRNA.
 DR EMBL; AJ294541; CAC08217.1; -; Genomic_DNA.
 DR PIR; B61318; B61318.
 DR PIR; JC4235; JC4235.
 DR PDB; 1CF5; X-ray; A/B=24-272.
 DR PDB; 1D8V; NMR; A=24-286.
 DR InterPro; IPRO01574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PRO0396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW 3D-structure; Antiviral protein; Direct protein sequencing;
 KW Glycoprotein; Hydrolase; Plant defense; Protein synthesis inhibitor;
 KW Signal; Toxin.
 FT SIGNAL 1 23
 FT CHAIN 24 286 Ribosome-inactivating protein beta-
 FT momorcharin.
 FT /FTId=PRO_0000030773.
 FT ACT_SITE 93 93 By similarity.
 FT ACT_SITE 132 132 By similarity.
 FT ACT_SITE 181 181 By similarity.
 FT ACT_SITE 184 184 By similarity.

FT	CARBOHYD	74	74	N-linked (GlcNAc. . .).
FT	CONFLICT	23	23	G -> M (in Ref. 3 and 4).
FT	CONFLICT	37	37	Y -> T (in Ref. 5).
FT	CONFLICT	67	67	S -> P (in Ref. 5).
FT	CONFLICT	147	147	D -> E (in Ref. 4).
FT	CONFLICT	188	188	I -> T (in Ref. 1).
FT	CONFLICT	228	228	G -> A (in Ref. 4).
FT	STRAND	25	28	
FT	HELIX	29	31	
FT	HELIX	34	45	
FT	TURN	46	47	
FT	STRAND	48	48	
FT	STRAND	50	54	
FT	TURN	55	56	
FT	STRAND	57	60	
FT	STRAND	62	63	
FT	TURN	66	67	
FT	STRAND	68	76	
FT	TURN	78	79	
FT	STRAND	82	88	
FT	TURN	89	91	
FT	STRAND	94	99	
FT	TURN	100	101	
FT	STRAND	102	106	
FT	TURN	107	108	
FT	HELIX	111	116	
FT	STRAND	117	118	
FT	TURN	119	120	
FT	STRAND	121	128	
FT	STRAND	130	131	
FT	HELIX	132	139	
FT	TURN	140	140	
FT	STRAND	141	141	
FT	HELIX	143	145	
FT	STRAND	146	146	
FT	STRAND	148	149	
FT	HELIX	150	161	
FT	TURN	162	162	
FT	TURN	165	167	
FT	HELIX	168	177	
FT	TURN	178	179	
FT	HELIX	180	184	
FT	STRAND	185	185	
FT	HELIX	186	194	
FT	STRAND	196	200	
FT	STRAND	204	204	
FT	HELIX	205	210	
FT	TURN	211	214	
FT	HELIX	215	222	
FT	TURN	223	228	
FT	STRAND	229	237	
FT	TURN	239	240	
FT	STRAND	241	241	
FT	STRAND	243	248	
FT	TURN	249	250	
FT	STRAND	251	251	
FT	HELIX	252	256	
FT	TURN	257	257	
FT	STRAND	258	258	
FT	STRAND	261	261	
FT	HELIX	264	269	
FT	TURN	270	271	
FT	TURN	274	276	
FT	TURN	279	281	
FT	STRAND	282	283	

SQ SEQUENCE 286 AA; 32031 MW; 6B2DF55A41D8F921 CRC64;

Query Match 27.3%; Score 348; DB 1; Length 286;
 Best Local Similarity 37.4%; Pred. No. 8.7e-21;
 Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;

Qy 5 VSFSTKGATYITYVNFINELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDNGQLA 64
 ! : | || || : : | | : || || | : | : | : | : | : :

Db 25 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISD-SRRFILLNLTSYAYETI 83

Qy 65 EIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-GEKAYR 123

Db :|||||:||||| :| :|||||::| || ||||| | :|:| :|:
84 SVAIDVTNVYVVAYRTRDVSYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAHKIR 143

Qy 124 ETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSAAARFTFIENQIRNNFQQ 183
| |||: | | . : | :|||:|| :||||| :|| |:
Db 144 ENIDLGLPALSSAI----TTLFYYNAQSAPSALLVLIQTTAEAAARFKYIERHVAKYVAT 198

Qy 184 RIRPANNITISLENKGKLSFQI-RTSGANGMFSEAVELERANGKKYYVTAVDQ--VKPKI 240
:| |||||:| || || | | | :| :|:|| | || |:
Db 199 NFKPNLAIISLENQWSALSKQIFLAQNQGGKFRNPVDLIKPTGERFQVTNVDSDVVKGNI 258

Qy 241 ALL 243
| |
Db 259 KLL 261

Search completed: July 20, 2006, 09:53:07
Job time : 259.197 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 2.rai.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:37:31 ; Search time 33.8063 Seconds
(without alignments)
649.885 Million cell updates/sec

Title: US-10-717-243-2
Perfect score: 1287
Sequence: 1 GLDTVSFSTKGATYITYVNF.....AVDQVKPKIALLKFVDKDPK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB	ID	Description
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1	1287	100.0	251	1	US-08-425-336-2	Sequence 2, Appli
2	1287	100.0	251	1	US-08-488-113B-2	Sequence 2, Appli
3	1287	100.0	251	1	US-08-477-484B-2	Sequence 2, Appli
4	1287	100.0	251	1	US-08-646-360-2	Sequence 2, Appli
5	1287	100.0	251	1	US-08-621-803-247	Sequence 247, App
6	1287	100.0	251	2	US-08-839-765-2	Sequence 2, Appli
7	1287	100.0	251	2	US-09-136-389-2	Sequence 2, Appli
8	1287	100.0	251	2	US-09-217-352-247	Sequence 247, App
9	1287	100.0	251	2	US-09-610-838-2	Sequence 2, Appli
10	1287	100.0	251	2	US-09-711-485-2	Sequence 2, Appli

11	1287	100.0	251	2	US-09-645-603B-2	Sequence 2, Appli
12	1284	99.8	251	1	US-07-901-707-2	Sequence 2, Appli
13	1284	99.8	251	1	US-07-988-430-2	Sequence 2, Appli
14	1284	99.8	251	5	PCT-US92-09487-2	Sequence 2, Appli
15	1284	99.8	293	1	US-08-621-803-259	Sequence 259, App
16	1284	99.8	293	2	US-09-217-352-259	Sequence 259, App
17	1284	99.8	309	1	US-08-621-803-253	Sequence 253, App
18	1284	99.8	309	2	US-09-217-352-253	Sequence 253, App
19	1284	99.8	332	1	US-08-621-803-251	Sequence 251, App
20	1284	99.8	332	2	US-09-217-352-251	Sequence 251, App
21	1282	99.6	251	1	US-08-425-336-108	Sequence 108, App
22	1282	99.6	251	1	US-08-488-113B-108	Sequence 108, App
23	1282	99.6	251	1	US-08-477-484B-108	Sequence 108, App
24	1282	99.6	251	1	US-08-646-360-108	Sequence 108, App
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28	1282	99.6	251	2	US-09-711-485-108	Sequence 108, App
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34	1279	99.4	251	1	US-08-488-113B-103	Sequence 103, App
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36	1279	99.4	251	1	US-08-488-113B-105	Sequence 105, App
37	1279	99.4	251	1	US-08-488-113B-106	Sequence 106, App
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42	1279	99.4	251	1	US-08-477-484B-106	Sequence 106, App
43	1279	99.4	251	1	US-08-477-484B-109	Sequence 109, App
44	1279	99.4	251	1	US-08-646-360-103	Sequence 103, App
45	1279	99.4	251	1	US-08-646-360-104	Sequence 104, App

ALIGNMENTS

RESULT 1
 US-08-425-336-2
; Sequence 2, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-2

Query Match 100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
|||
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Qy 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQM VSEAARFTFIENQIRNN 180
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Db 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQM VSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANN TISLEN KWGKLSF QIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
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Db 181 FQQRIRPANN TISLEN KWGKLSF QIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
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Db 241 ALLKFVDKDPK 251

RESULT 2
US-08-488-113B-2
; Sequence 2, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992

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; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/901,707
;   FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/787,567
;   FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: McNicholas, Janet M.
;   REGISTRATION NUMBER: 32,918
;   REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312/707-8889
;   TELEFAX: 312/707-9155
;   TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 251 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-488-113B-2

Query Match          100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      241 ALLKFVDKDPK 251
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Db      241 ALLKFVDKDPK 251

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RESULT 3
US-08-477-484B-2
; Sequence 2, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336

; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-477-484B-2

Query Match 100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

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Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 4
US-08-646-360-2
; Sequence 2, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-360-2

Query Match 100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFVGSYPSLEGEK 120
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GQLAEIAIDVTSVVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFVGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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Db 121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
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Db 241 ALLKFVDKDPK 251

RESULT 5
US-08-621-803-247
; Sequence 247, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America

; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-621-803-247

RESULT 6

; Sequence 2, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997

; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-839-765-2

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDCPGKCFVLVALSNDN 60
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Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDCPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFHGGSYPSLEGEK 120
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|||...|||||...|||||...|||||...|||||...|||||...
Db 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTS GANGMFSEAVELERANGKYYVTAVDQVKPKI 240
|||...|||||...|||||...|||||...|||||...|||||...
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTS GANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
|||...|||||...
Db 241 ALLKFVDKDPK 251

RESULT 7
US-09-136-389-2
; Sequence 2, Application US/09136389 ,
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-136-389-2

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db	1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Qy	61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
Db	61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
Qy	121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180
Db	121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180
Qy	181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db	181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Qy	241 ALLKFVDKDPK 251
Db	241 ALLKFVDKDPK 251

RESULT 8

US-09-217-352-247

; Sequence 247, Application US/09217352
; Patent No. 6274344
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,352
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-217-352-247

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVIVALSNNDN 60
|||
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVIVALSNNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
|||
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVIQMVSEAARFTFIENQIRNN 180
|||
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVIQMVSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
|||
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
|||
Db 241 ALLKFVDKDPK 251

RESULT 9
US-09-610-838-2
; Sequence 2, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-610-838-2

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Query Match          100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GLDTVSFSTKGATIYTIVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 GLDTVSFSTKGATIYTIVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

Qy      61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy      121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVIQMVSearftfienqirnn 180
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVIQMVSearftfienqirnn 180

Qy      181 FQQIRPANNTI SLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 FQQIRPANNTI SLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy      241 ALLKFVDKDPK 251
        ||||||| | | |
Db      241 ALLKFVDKDPK 251

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RESULT 10
US-09-711-485-2
; Sequence 2, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-711-485-2

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db |||||||
Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
Db |||||||
Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db |||||||
Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db |||||||
Qy 241 ALLKFVDKDPK 251
Db |||||||
Qy 241 ALLKFVDKDPK 251

RESULT 11
US-09-645-603B-2
; Sequence 2, Application US/09645603B
; Patent No. 6652861
; GENERAL INFORMATION:
; APPLICANT: LEE-HUANG, Sylvia
; TITLE OF INVENTION: Anti-HIV and Anti-tumor Peptides and Truncated Polypeptides of
; TITLE OF INVENTION: map30 and gap31
; FILE REFERENCE: LEE-HUANG 4A
; CURRENT APPLICATION NUMBER: US/09/645,603B
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/150,885
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Gelonium multiflorum
US-09-645-603B-2

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVIVALSNNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVIVALSNNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK. 120
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 12
US-07-901-707-2
; Sequence 2, Application US/07901707
; Patent No. 5376546
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Steve F.
; APPLICANT: Lane, Julie A.
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,707
; FILING DATE: 19920619
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein

RESULT 13

US-07-988-430-2

; Sequence 2, Application US/07988430

; Patent No. 5416202

; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping

; ATTACHMENT: See, shaded ring
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall

; ADDRESSEE: Bicknell

; STREET: Two Fi

; STREET: Street

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA
; SIP: 60603

; ZIP: 60603
; COMPUTER READ

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOSE/MS-DOS

OPERATING SYSTEM: PC-DOSS/MS-DOS
SOFTWARE: PatentIn Release #1.0 Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/988,430

FILING DATE: 19921209

CLASSIFICATION: 435

; . PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-988-430-2

Query Match 99.8%; Score 1284; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-124;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 14
PCT-US92-09487-2
; Sequence 2, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-09487-2

Query Match 99.8%; Score 1284; DB 5; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.7e-124;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db |||||||
Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db |||||||
Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db |||||||:|||||||
Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSLEGEK 120
Db |||||||:|||||||
Qy 121 AYRETTDLGIEPLRIGIKKLDENAINDKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db |||||||:|||||||
Qy 121 AYRETTDLGIEPLRIGIKKLDENAINDKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db |||||||:|||||||
Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db |||||||:|||||||
Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db |||||||:|||||||
Qy 241 ALLKFVDKDPK 251
Db |||||||
Qy 241 ALLKFVDKDPK 251

RESULT 15
US-08-621-803-259
; Sequence 259, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
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; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 259:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-621-803-259

Query Match 99.8%; Score 1284; DB 1; Length 293;
Best Local Similarity 99.6%; Pred. No. 3.4e-124;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db 23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 82

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSEGEK 120
Db 83 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSEGEK 142

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db 143 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 202

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 203 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 262

Qy 241 ALLKFVDKDPK 251
Db 263 ALLKFVDKDPK 273

Search completed: July 20, 2006, 09:38:55
Job time : 33.8063 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 2.rag.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:35:59 ; Search time 203.301 Seconds
(without alignments)
564.490 Million cell updates/sec

Title: US-10-717-243-2
Perfect score: 1287
Sequence: 1 GLDTVSFSTKGATYITYVNF.....AVDQVKPKIALLKFVDKDPK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:
9: geneseqp2005s:
10: geneseqp2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB	ID	Description
1	1287	100.0	251	2 AAR63903	Aar63903 Type I ri
2	1287	100.0	251	8 ADG63044	Adg63044 Gelonium
3	1287	100.0	316	5 ABG71551	Abg71551 G. multif
4	1287	100.0	498	9 AEB68722	Aeb68722 scFv23-ge
5	1287	100.0	507	5 ABG71552	Abg71552 Murine sc
6	1284	99.8	293	2 AAW29300	Aaw29300 BPI pepti
7	1284	99.8	309	2 AAW29303	Aaw29303 BPI pepti

8	1284	99.8	332	2	AAW29294	Aaw29294 BPI pepti
9	1283	99.7	751	9	AEC95468	Aec95468 Ep-CAM-ta
10	1282	99.6	251	2	AAR63923	Aar63923 Type I RI
11	1279	99.4	251	2	AAR63921	Aar63921 Type I RI
12	1279	99.4	251	2	AAR63918	Aar63918 Type I RI
13	1279	99.4	251	2	AAR63920	Aar63920 Type I RI
14	1279	99.4	251	2	AAR63919	Aar63919 Type I RI
15	1279	99.4	251	2	AAR63924	Aar63924 Type I RI
16	1278	99.3	251	2	AAR63922	Aar63922 Type I RI
17	1278	99.3	251	2	AAR63917	Aar63917 Type I RI
18	1278	99.3	251	2	AAR63912	Aar63912 Type I RI
19	1275	99.1	251	2	AAR74177	Aar74177 Type I ri
20	1269	98.6	251	2	AAR37291	Aar37291 Plant typ
21	1269	98.6	251	2	AAR63914	Aar63914 Type I RI
22	1261	98.0	251	2	AAR63915	Aar63915 Type I RI
23	1252	97.3	251	2	AAR63916	Aar63916 Type I RI
24	1242.5	96.5	258	2	AAR22227	Aar22227 Gelonin t
25	1219.5	94.8	513	9	AEC95310	Aec95310 Murine sF
26	1208	93.9	506	9	AEB68720	Aeb68720 scFv23-ge
27	1176	91.4	235	2	AAR63913	Aar63913 Type I RI
28	346	26.9	263	2	AAR63905	Aar63905 Type I ri
29	346	26.9	263	2	AAR74179	Aar74179 Type I ri
30	346	26.9	263	8	ADG63043	Adg63043 Momordica
31	344	26.7	565	1	AAP50166	Aap50166 Sequence
32	344	26.7	565	4	AAG78300	Aag78300 Castor be
33	344	26.7	574	1	AAP70325	Aap70325 Sequence
34	343	26.7	267	2	AAR30722	Aar30722 Ricin A f
35	343	26.7	267	2	AAR37290	Aar37290 Ricin A c
36	343	26.7	267	2	AAR63902	Aar63902 Ricin A-c
37	343	26.7	267	3	AAB19265	Aab19265 Amino aci
38	343	26.7	267	7	ADC24288	Adc24288 Ricin tox
39	343	26.7	268	2	AAR39570	Aar39570 Sequence
40	343	26.7	268	10	AEF18884	Aef18884 Ricin, SE
41	343	26.7	290	2	AAW21699	Aaw21699 Ricin A-c
42	343	26.7	290	2	AAW25136	Aaw25136 Ricin A-c
43	343	26.7	332	1	AAP70097	Aap70097 Ricin A.
44	343	26.7	332	1	AAP70838	Aap70838 Sequence
45	343	26.7	332	1	AAP95639	Aap95639 Ricin A e

ALIGNMENTS

RESULT 1
AAR63903
ID AAR63903 standard; protein; 251 AA.
XX
AC AAR63903;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I ribosome-inactivating protein gelonin.
XX
KW Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS *Gelonium multiflorum*.
XX
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
DR N-PSDB; AAQ75532.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which

PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 1; Fig 1; 221pp; English.
XX
CC AAQ75532 encodes AAR63903 type I ribosome-inactivating protein (RIP)
CC gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key
CC components of cytotoxic therapeutic agents (CTAs), which include gene
CC fusion products and immunoconjugates. CTAs may be used to selectively
CC eliminate any cell type to which a RIP component is targeted, by the
CC specific binding capacity of the second component of the agent. They can
CC be used in the treatment of diseases where the elimination of a
CC particular cell type is desired, such as autoimmune disease, cancer and
CC graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.9e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLLVVIQMVEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLLVVIQMVEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 2
ADG63044
ID ADG63044 standard; protein; 251 AA.
XX
AC ADG63044;
XX
DT 11-MAR-2004 (first entry)
XX
DE Gelonium anti-HIV protein 31kDa (GAP31).
XX
KW anti-HIV; cytostatic; peptide therapy; anti-tumour; antiviral; MAP30;
KW GAP31; HIV; tumour; gelonium anti-HIV protein 31kDa.
XX
OS Gelonium multiflorum.
XX
PN US6652861-B1.
XX
PD 25-NOV-2003.
XX
PF 25-AUG-2000; 2000US-00645603.
XX
PR 26-AUG-1999; 99US-0150885P.
XX
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Lee-Huang S;
XX
DR WPI; 2004-050519/05.
XX
PT New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and
PT antiviral activity, useful for treating human immunodeficiency virus
PT infection or tumor.
XX
PS Example 1; SEQ ID NO 2; 22pp; English.
XX

CC The invention describes an isolated peptide or polypeptide having an anti
CC -tumour and antiviral activity. Also described is a composition
CC comprising the isolated peptide or polypeptide, and a carrier, excipient
CC or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides or
CC polypeptides. The peptide or polypeptide is useful for treating HIV
CC infection, and tumour. This is the amino acid sequence of Gelonium anti-
CC HIV protein 30kDa (MAP30).

XX

SQ Sequence 251 AA;

Query Match 100.0%; Score 1287; DB 8; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.9e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 3

ABG71551

ID ABG71551 standard; protein; 316 AA.

XX

AC ABG71551;

XX

DT 08-JAN-2003 (first entry)

XX

DE G. multiflorum recombinant gelonin (rGel) toxin.

XX

KW Modified protein; reduced antigenicity; modified toxin; gelonin;
KW designer toxin; immunotoxin; proteinaceous compound; cancer;
KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
KW inflammatory disease; cardiovascular disease; diabetes;
KW pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
KW cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
KW recombinant gelonin; rGel.

XX

OS Gelonium multiflorum.

XX

PN WO200269886-A2.

XX

PD 12-SEP-2002.

XX

PF 12-FEB-2002; 2002WO-US004195.

XX

PR 12-FEB-2001; 2001US-0268402P.

XX

PA (RERE-) RES DEV FOUND.

XX

PI Rosenblum MG, Cheung L;

XX

DR WPI; 2002-750431/81.

DR N-PSDB; ABS56021.

XX

PT Generating a modified protein with reduced antigenicity for treating
PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region
PT antigenic in the first subject using antiserum from either the first or a
PT second subject.

XX

PS Claim 63; Page 169-170; 176pp; English.

XX

CC The present invention relates to a method of generating a modified
CC protein with reduced antigenicity while maintaining its biological
CC activity. The method comprises identifying a region of the protein that
CC is antigenic in a first subject using antiserum from either the first
CC subject or a second subject of the same species as the first subject. In
CC particular the invention discloses modified toxin compounds, for example
CC gelonin toxin derived from *Gelonium multiflorum*, that are truncated
CC and/or possess reduced antigenicity. Such designer toxins have
CC therapeutic, diagnostic, and preventative benefits, particularly as
CC immunotoxins. The method of the invention is useful for generating
CC proteinaceous compounds with less antigenicity. The immunotoxin and
CC gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
CC skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
CC bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
CC bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
CC compositions of the invention are also useful for treating microbial
CC pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
CC diseases, hyperproliferative disorders including cancer, leukaemias,
CC arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
CC diseases, and diabetes. The method provides less antigenic proteins,
CC peptides and polypeptides, which are more effective than prior art. The
CC present sequence represents *G. multiflorum* recombinant gelonin (rGel)

XX

SQ Sequence 316 AA;

Query Match 100.0%; Score 1287; DB 5; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.7e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVIVALSNNDN 60
Db 47 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVIVALSNNDN 106

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 107 GQLAEIAIDVTSVYVVGYQVRNRSSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 166

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db 167 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 226

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 227 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 286

Qy 241 ALLKFVDKDPK 251
Db 287 ALLKFVDKDPK 297

RESULT 4

AEB68722

ID AEB68722 standard; protein; 498 AA.

XX AC AEB68722;

XX DT 06-OCT-2005 (first entry)

XX DE scFv23-gelonin immunotoxin amino acid sequence SEQ ID NO:13.

XX KW antibody engineering; c-erbB-2 protein; toxin; gelonin; cytostatic;

KW immunotoxin; neoplasm.

XX OS Synthetic.

XX PN US2005163774-A1.

XX PD 28-JUL-2005.

XX PF 13-OCT-2004; 2004US-00964195.

XX PR 10-APR-1992; 92US-00867728.

PR 09-DEC-1993; 93US-00164638.

PR 02-SEP-1994; 94US-00300082.

PR 17-MAR-1995; 95US-00404499.
PR 26-MAY-1999; 99US-00320156.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Rosenblum M, Shawver LK;
XX
DR WPI; 2005-561813/57.
DR N-PSDB; AEB68721.
XX
PT New immunotoxins directed against c-erbB-2 related surface antigens,
PT useful for treating neoplastic diseases, e.g. carcinoma or
PT adenocarcinoma.
XX
PS Disclosure; SEQ ID NO 13; 60pp; English.
XX

CC The invention relates to a composition comprising a conjugate of an
CC antibody exhibiting binding specificity for an extracellular epitope of c
CC -erbB-2 protein and a plant derived toxin, where the toxin is
CC pharmacologically effective against neoplastic cells and is selected from
CC gelonin, full length recombinant gelonin, functional gelonin fragments or
CC functional gelonin derivatives. Also described is a pharmaceutical
CC composition comprising the composition above and a pharmaceutical
CC vehicle. For treating neoplastic diseases, e.g. human mammary carcinomas,
CC human ovarian carcinomas, lung carcinomas, gastric tumors, salivary gland
CC adenocarcinomas, or colon adenocarcinomas. The present sequence
CC represents a scFv23-gelonin amino acid sequence, which is used in an
CC example from the present invention.
XX
SQ Sequence 498 AA;

Query Match 100.0%; Score 1287; DB 9; Length 498;
Best Local Similarity 100.0%; Pred. No. 5.2e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVILVALSNDN 60
Db 247 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVILVALSNDN 306

Qy 61 GQLAEIAIDVTSVVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 307 GQLAEIAIDVTSVVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 366

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db 367 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 426

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 427 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 486

Qy 241 ALLKFVDKDPK 251
Db 487 ALLKFVDKDPK 497

RESULT 5
ABG71552
ID ABG71552 standard; protein; 507 AA.
XX
AC ABG71552;
XX
DT 08-JAN-2003 (first entry)
XX
DE Murine scfvMEL/G. multiflorum rGel fusion protein.
XX
KW Modified protein; reduced antigenicity; modified toxin; gelonin;
KW designer toxin; immunotoxin; proteinaceous compound; cancer;
KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
KW inflammatory disease; cardiovascular disease; diabetes;
KW pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
KW cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
KW murine; single-chain ZME-018 antibody; recombinant gelonin; rGel;
KW scfvMEL/rGel; mutant; mutein.
XX

OS Mus sp.
OS Gelonium multiflorum.
OS Synthetic.
OS Chimeric.
XX
PN WO200269886-A2.
XX
PD 12-SEP-2002.
XX
PF 12-FEB-2002; 2002WO-US004195.
XX
PR 12-FEB-2001; 2001US-0268402P.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Rosenblum MG, Cheung L;
XX
DR WPI; 2002-750431/81.
DR N-PSDB; ABS56029.
XX
PT Generating a modified protein with reduced antigenicity for treating
PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region
PT antigenic in the first subject using antiserum from either the first or a
PT second subject.
XX
PS Disclosure; Page 174-176; 176pp; English.
XX
CC The present invention relates to a method of generating a modified
CC protein with reduced antigenicity while maintaining its biological
CC activity. The method comprises identifying a region of the protein that
CC is antigenic in a first subject using antiserum from either the first
CC subject or a second subject of the same species as the first subject. In
CC particular the invention discloses modified toxin compounds, for example
CC gelonin toxin derived from Gelonium multiflorum, that are truncated
CC and/or possess reduced antigenicity. Such designer toxins have
CC therapeutic, diagnostic, and preventative benefits, particularly as
CC immunotoxins. The method of the invention is useful for generating
CC proteinaceous compounds with less antigenicity. The immunotoxin and
CC gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
CC skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
CC bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
CC bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
CC compositions of the invention are also useful for treating microbial
CC pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
CC diseases, hyperproliferative disorders including cancer, leukaemias,
CC arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
CC diseases, and diabetes. The method provides less antigenic proteins,
CC peptides and polypeptides, which are more effective than prior art. The
CC present sequence represents murine single-chain ZME-018 antibody/G.
CC multiflorum recombinant gelonin (rGel) (scfvMEL/rGel) fusion protein
XX
SQ Sequence 507 AA;

Query Match 100.0%; Score 1287; DB 5; Length 507;
Best Local Similarity 100.0%; Pred. No. 5.3e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db 257 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 316

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 317 GQLAEIAIDVTSVYVVGYQVRNRSSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 376

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db 377 AYRETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 436

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 437 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 496

Qy 241 ALLKFVDKDPK 251
Db 497 ALLKFVDKDPK 507

RESULT 6
AAW29300
ID AAW29300 standard; protein; 293 AA.
XX
AC AAW29300;
XX
DT 20-APR-1998 (first entry)
XX
DE BPI peptide fusion protein pING3797 vector construct protein.
XX
KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
KW fungicidal; recombinant DNA; vector.
XX
OS Synthetic.
OS Pectobacterium carotovorum.
OS Homo sapiens.
OS Chimeric.
XX
PN WO9735009-A1.
XX
PD 25-SEP-1997.
XX
PF 18-MAR-1997; 97WO-US005287.
XX
PR 22-MAR-1996; 96US-00621803.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD;
XX
DR WPI; 1997-480215/44.
DR N-PSDB; AAT86336.
XX
PT Recombinant production of bactericidal/permeability increasing protein -
PT by expression as a fusion protein in microbial host cells, then cleaving
PT the BPI peptide from the carrier.
XX
PS Example 1; Page 160-161; 186pp; English.
XX
CC A new recombinant DNA vector construct has been developed which encodes a
CC fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents the protein
CC from the pING3797 vector construct which codes for a BPI fusion protein.
CC The peptides have many uses including the treatment of bacterial and
CC fungal infections. BPI peptides also bind to endotoxins and heparin,
CC neutralising their effects. The peptides have further been shown to
CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion
CC proteins have been found to be expressed in large amounts without
CC significant proteolysis, and in some cases are actually secreted from the
CC host cells. This allows the indirect production of anti-microbial BPI
CC peptides in microbial hosts
XX
SQ Sequence 293 AA;

Query Match 99.8%; Score 1284; DB 2; Length 293;
Best Local Similarity 99.6%; Pred. No. 4.9e-125;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVFSFKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db 23 GLDTVFSFKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 82

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 83 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSSLEGEK 142

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180
Db 143 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 202

Qy 181 FQQRIRPANNNTISLENKKGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 240
 |||||||
 Db 203 FQQRIRPANNNTISLENKKGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 262
 |||||||
 Qy 241 ALLKFVDKDPK 251
 |||||||
 Db 263 ALLKFVDKDPK 273

RESULT 7
 AAW29303
 ID AAW29303 standard; protein; 309 AA.
 XX
 AC AAW29303;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE BPI peptide fusion protein pING3795 vector construct protein.
 XX
 KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
 KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
 KW fungicidal; recombinant DNA; vector.
 XX
 OS Synthetic.
 OS Pectobacterium carotovorum.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN WO9735009-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 18-MAR-1997; 97WO-US005287.
 XX
 PR 22-MAR-1996; 96US-00621803.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Better MD;
 XX
 DR WPI; 1997-480215/44.
 DR N-PSDB; AAT86341.
 XX
 PT Recombinant production of bactericidal/permeability increasing protein -
 PT by expression as a fusion protein in microbial host cells, then cleaving
 PT the BPI peptide from the carrier.
 XX
 PS Example 1; Page 152-153; 186pp; English.
 XX
 CC A new recombinant DNA vector construct has been developed which encodes a
 CC fusion protein and is suitable for introduction into a bacterial host.
 CC The vector comprises: (a) DNA encoding at least one cationic
 CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
 CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
 CC located between (a) and (b). The present sequence represents the protein
 CC from the pING3795 vector construct which codes for a BPI fusion protein.
 CC The peptides have many uses including the treatment of bacterial and
 CC fungal infections. BPI peptides also bind to endotoxins and heparin,
 CC neutralising their effects. The peptides have further been shown to
 CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion
 CC proteins have been found to be expressed in large amounts without
 CC significant proteolysis, and in some cases are actually secreted from the
 CC host cells. This allows the indirect production of anti-microbial BPI
 CC peptides in microbial hosts
 XX
 SQ Sequence 309 AA;

 Query Match 99.8%; Score 1284; DB 2; Length 309;
 Best Local Similarity 99.6%; Pred. No. 5.3e-125;
 Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
 |||||||
 Db 23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 82

 Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120

Db :|||||||||||||||||||||||||||||||||||||||||:|||||||
83 GQLAEIAIDVTSVYVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSEGEK 142
Qy 121 AYRETTDLGIEPLRIGIKKKDENAIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180
Db :|||||||||||||||||||||||||||||||||||||
143 AYRETTDLGIEPLRIGIKKKDENAIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 202
Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db :|||||||||||||||||||||||||||||||||
203 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 262
Qy 241 ALLKFVDKDPK 251
Db :|||||||||
263 ALLKFVDKDPK 273

RESULT 8
AAW29294

ID AAW29294 standard; protein; 332 AA.
XX
AC AAW29294;
XX
DT 20-APR-1998 (first entry)
XX
DE BPI peptide fusion protein pING3793 vector construct protein.
XX
KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
KW fungicidal; recombinant DNA; vector.
XX
OS Synthetic.
OS Pectobacterium carotovorum.
OS Homo sapiens.
OS Chimeric.
XX
PN WO9735009-A1.
XX
PD 25-SEP-1997.
XX
PF 18-MAR-1997; 97WO-US005287.
XX
PR 22-MAR-1996; 96US-00621803.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD;
XX
DR WPI; 1997-480215/44.
DR N-PSDB; AAT86332.
XX
PT Recombinant production of bactericidal/permeability increasing protein -
PT by expression as a fusion protein in microbial host cells, then cleaving
PT the BPI peptide from the carrier.
XX
PS Example 1; Page 148-150; 186pp; English.
XX
CC A new recombinant DNA vector construct has been developed which encodes a
CC fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents the protein
CC from the pING3793 vector construct which codes for a BPI fusion protein.
CC The peptides have many uses including the treatment of bacterial and
CC fungal infections. BPI peptides also bind to endotoxins and heparin,
CC neutralising their effects. The peptides have further been shown to
CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion
CC proteins have been found to be expressed in large amounts without
CC significant proteolysis, and in some cases are actually secreted from the
CC host cells. This allows the indirect production of anti-microbial BPI
CC peptides in microbial hosts
XX
SQ Sequence 332 AA;

Query Match 99.8%; Score 1284; DB 2; Length 332;
Best Local Similarity 99.6%; Pred. No. 5.9e-125;

Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
 |||||
 Db 23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 82

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
 |||||
 Db 83 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSLEGEK 142

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVMSEAARFTFIENQIRNN 180
 |||||
 Db 143 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVMSEAARFTFIENQIRNN 202

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
 |||||
 Db 203 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 262

Qy 241 ALLKFVDKDPK 251
 |||||||
 Db 263 ALLKFVDKDPK 273

RESULT 9

AEC95468

ID AEC95468 standard; protein; 751 AA.

XX

AC AEC95468;

XX

DT 01-DEC-2005 (first entry)

XX

DE Ep-CAM-targeted-modified bouganin VB6-845-gelonin.

XX

KW cytostatic; gene therapy; cytotoxin; immune stimulation; pharmaceutical;
 KW colorectal tumor; breast tumor; ovary tumor; pancreas tumor;
 KW head & neck tumor; bladder tumor; renal tumor; melanoma;
 KW gastrointestinal tumor; prostate tumor; lung tumor;
 KW small-cell lung cancer; sarcoma; glioma; lymphoma; neoplasm; bouganin;
 KW VB6-845-gelonin.

XX

OS Bougainvillea spectabilis.

OS Synthetic.

XX

PN WO2005090579-A1.

XX

PD 29-SEP-2005.

XX

PF 18-MAR-2005; 2005WO-CA000410.

XX

PR 19-MAR-2004; 2004US-0554580P.

PR 26-NOV-2004; 2004US-0630571P.

XX

PA (BAKE//) BAKER M.

PA (CARR//) CARR F J.

PA (HELL//) HELLEDOORN K.

PA (CIZE//) CIZEAU J.

PA (MACD//) MACDONALD G C.

PA (ENTW//) ENTWISTLE J.

PA (BOSC//) BOSC D G.

PA (GLOV//) GLOVER N R.

XX

PI Baker M, Carr FJ, Hellendoorn K, Cizeau J, Macdonald GC;

PI Entwistle J, Bosc DG, Glover NR;

XX

DR WPI; 2005-649604/66.

DR N-PSDB; AEC95467.

XX

PT New modified bouganin protein having reduced propensity to activate an
 PT immune response, for treating cancer, e.g. colorectal cancer, breast
 PT cancer, ovarian cancer, or head and neck cancer.

XX

PS Example 7; SEQ ID NO 26; 190pp; English.

XX

CC The invention describes a modified bouganin protein, where the modified
 CC bouganin has a reduced propensity to activate an immune response. Also
 CC described are: a cytotoxin comprising: (a) a targeting group attached to

CC (b) the new modified bouganin protein; or (c) a ligand that binds to a
CC cancer cell attached to: (d) the modified bouganin protein; a
CC pharmaceutical composition comprising the cytotoxin and a pharmaceutical
CC carrier, diluent, or excipient; a process of preparing a pharmaceutical
CC for treating an animal with cancer; a T-cell epitope comprising a fully
CC defined 15 amino acid sequence (SEQ ID NO: 2, 3, or 4); and a nucleic
CC acid molecule encoding the modified bouganin, the cytotoxin, or the T-
CC cell epitope peptide. Ala-Lys-Val-Asp-Arg-Lys-Asp-Leu-Glu-Leu-Gly-Val-Tyr
CC -Lys-Leu (epitope region R1, SEQ ID NO: 2) Leu-Gly-Val-Tyr-Lys-leu-Glu-
CC Phe-Ser-Ile-Glu-Ala-Ile-His-Gly (epitope region R2, SEQ ID NO: 3) Asn-Gly
CC -Gln-Glu-Ile-Ala-Lys-Phe-Leu-Ile-Val-Ile-Gln-Met (epitope region R3,
CC SEQ ID NO: 4). Also disclosed are methods for inhibiting or destroying
CC cancer cells, and treating cancer. The cytotoxin is useful in the
CC manufacture of a medicament for inhibiting or destroying a cancer cell or
CC for treating cancer selected from colorectal cancer, breast cancer,
CC ovarian cancer, pancreatic cancer, head and neck cancer, bladder cancer,
CC liver cancer, renal cancer, melanomas, gastrointestinal cancer, prostate
CC cancer, small cell and non small cell lung cancer, sarcomas, gliomas, or
CC T- and B-cell lymphomas. The bouganin protein, cytotoxins, compositions,
CC and methods are useful for treating various forms of the cancer given.
CC This is the amino acid sequence of a modified Bougainvillea spectabilis
CC mature bouganin protein.

XX

SQ Sequence 751 AA;

Query Match 99.7%; Score 1283; DB 9; Length 751;
Best Local Similarity 99.6%; Pred. No. 2.5e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVILVALSNDN 60
Db 254 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVILVALSNDN 313

Qy 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHF GG SYP SLEGEK 120
Db 314 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHF GG SYP SLEGEK 373

Qy 121 AYRETTDLGIEPLRIGIKKLDENAI DNYKPTEIASSLLVVIQM VSEAARFTFIENQIRNN 180
Db 374 AYRETTDLGIEPLRIGIKKLDENAI DNYKPTEIASSLLVVIQM VSEAARFTFIENQIRNN 433

Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 434 FQQRIRPTNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 493

Qy 241 ALLKFVDKDPK 251
Db 494 ALLKFVDKDPK 504

RESULT 10

AAR63923

ID AAR63923 standard; protein; 251 AA.

XX

AC AAR63923;

XX

DT 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

XX

DE Type I RIP gelonin analog Gel(C103).

XX

KW Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.

XX

OS Gelonium multiflorum.

XX

PN WO9426910-A1.

XX

PD 24-NOV-1994.

XX

PF 12-MAY-1994; 94WO-US005348.

XX

PR 12-MAY-1993; 93US-00064691.

XX

PA (XOMA) XOMA CORP.

XX
 PI Better MD, Carroll SF, Studnicka GM;
 XX
 DR WPI; 1995-006804/01.
 XX
 PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 PT are suitable for use as components of cytotoxic therapeutic agents.
 XX
 PS Example 3; Page 187-188; 221pp; English.
 XX
 CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targetted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 251 AA;

 Query Match 99.6%; Score 1282; DB 2; Length 251;
 Best Local Similarity 99.6%; Pred. No. 6.4e-125;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVIVALSNDN 60
 |||||||
 Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVIVALSNDN 60

 Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
 |||||||
 Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTCKTRLHFGGSYPSEGEK 120

 Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
 |||||||
 Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

 Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 |||||||
 Db 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

 Qy 241 ALLKFVDKDPK 251
 |||||||
 Db 241 ALLKFVDKDPK 251

RESULT 11
 AAR63921
 ID AAR63921 standard; protein; 251 AA.
 XX
 AC AAR63921;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)
 XX
 DE Type I RIP gelonin analog Gel(C10).
 XX
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.
 XX
 OS Gelonium multiflorum.
 XX
 PN WO9426910-A1.
 XX
 PD 24-NOV-1994.
 XX
 PF 12-MAY-1994; 94WO-US005348.
 XX
 PR 12-MAY-1993; 93US-00064691.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Better MD, Carroll SF, Studnicka GM;

XX
 DR WPI; 1995-006804/01.
 XX
 PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 PT are suitable for use as components of cytotoxic therapeutic agents.
 XX
 PS Example 3; Page 186; 221pp; English.
 XX
 CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targetted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 251 AA;

 Query Match 99.4%; Score 1279; DB 2; Length 251;
 Best Local Similarity 99.6%; Pred. No. 1.3e-124;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1 GLDTVSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

 Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

 Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

 Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 181 FQQRIRPANNNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

 Qy 241 ALLKFVDKDPK 251
 ||||||| |||||
 Db 241 ALLKFVDKDPK 251

RESULT 12
 AAR63918
 ID AAR63918 standard; protein; 251 AA.
 XX
 AC AAR63918;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)
 XX
 DE Type I RIP gelonin analog Gel(C248).
 XX
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.
 XX
 OS *Gelonium multiflorum*.
 XX
 PN WO9426910-A1.
 XX
 PD 24-NOV-1994.
 XX
 PF 12-MAY-1994; 94WO-US005348.
 XX
 PR 12-MAY-1993; 93US-00064691.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Better MD, Carroll SF, Studnicka GM;
 XX
 DR WPI; 1995-006804/01.

XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 183-184; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targetted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 99.4%; Score 1279; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.3e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKGWLKFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 FQQRIRPANNTISLENKGWLKFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
 ||||||| |||
Db 241 ALLKFVDCDPK 251

RESULT 13
AAR63920
ID AAR63920 standard; protein; 251 AA.
XX
AC AAR63920;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel(C244).
XX
KW Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
PN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which

PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 185; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targetted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Séquence 251 AA;

SQ Sequence 251 AA;

RESULT 14

AAR63919

ID AAR63919

xx

AC AAR63919;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)

27-002 1998 (FIRST ENTRY)
XX

DE

XX Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.

xx graft versus host disease

os

xx

PN WO9426910-A1.

XX

PD 24-NOV-1994.

RE 13 MAY 1984 84HQ 150053

PP 12-MAY-1994; 94WU-05005348.
XX

PR 12-MAY-1993; 93U

xx

PA (XOMA) XOMA CORP.

xx

PI Better MD, Carroll
xx

xx

DR WPI; 1995-006804/01.
XX

PT

PT Polynucleotide(s), encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.

PS Example 3; Page 184; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targetted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)

xx SO Sequence 251 AA:

```

Query Match          99.4%; Score 1279; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.3e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLRKCDPGKCFVLVALSNDN 60
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLRKCDPGKCFVLVALSNDN 60

Qy      61 GQLAEIAIDVTSVYVVGYQVRNRNSYFFKDAPDAAYEGLFKNTIKTRLHFVGGSYPSLEGEK 120
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db      61 GQLAEIAIDVTSVYVVGYQVRNRNSYFFKDAPDAAYEGLFKNTIKTRLHFVGGSYPSLEGEK 120

Qy      121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db      121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

Qy      181 FQQRIRPANNTISLENWKWGLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db      181 FQQRIRPANNTISLENWKWGLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPCI 240

Qy      241 ALLKFVDKDPK 251
        ||||||| |||||
Db      241 ALLKFVDKDPK 251

```

RESULT 15
AAR63924

ID AAR63924 standard; protein; 251 A
xx

AC AAB63924

xx

DT 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

xx

DE

XX
THE UNIVERSITY OF TORONTO LIBRARIES

KW
KWT

KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX

05

xx

PN

xx

PD
151

xx
REF 13-MAY-1994 : 84WO-US005348

xx

PR 12-MAY-1993: 93US-00064691

xx

PA (XOMA) XOMA CORP.

xx

PI Better MD, Carroll

xx

DR WP1; 1995-006804/01.
xx

PT

PT polyribonucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX

PS

XX

CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targetted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX

SQ Sequence 251 AA;

Query Match 99.4%; Score 1279; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.3e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db	1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Qy	61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db	61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Qy	121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180
Db	121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180
Qy	181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db	181 FQQCIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Qy	241 ALLKFVDKDPK 251
Db	241 ALLKFVDKDPK 251

Search completed: July 20, 2006, 09:43:42
Job time : 205.301 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 2.rapbm.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10717243 and Search Result us-10-717-243-2.rapbm.

[start](#)

[Go Back to previous page](#)

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:40:12 ; Search time 81.5055 Seconds
(without alignments)
1426.491 Million cell updates/sec

Title: US-10-717-243-2
Perfect score: 1287
Sequence: 1 GLDTVSFSTKGATYITYVNF.....AVDQVKPKIALLKFVDKDPK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1287	100.0	251	3	US-09-765-527-247	Sequence 247, Appl
2	1287	100.0	251	4	US-10-127-890-2	Sequence 2, Appl
3	1287	100.0	251	5	US-10-717-243-2	Sequence 2, Appl
4	1287	100.0	316	4	US-10-074-596-1	Sequence 1, Appl
5	1287	100.0	498	5	US-10-964-195-13	Sequence 13, Appl
6	1287	100.0	507	4	US-10-074-596-11	Sequence 11, Appl
7	1284	99.8	293	3	US-09-765-527-259	Sequence 259, App
8	1284	99.8	309	3	US-09-765-527-253	Sequence 253, App
9	1284	99.8	332	3	US-09-765-527-251	Sequence 251, App
10	1283	99.7	751	6	US-11-084-080-26	Sequence 26, Appl
11	1282	99.6	251	4	US-10-127-890-108	Sequence 108, App

12	1282	99.6	251	5	US-10-717-243-108	Sequence 108, App
13	1279	99.4	251	4	US-10-127-890-103	Sequence 103, App
14	1279	99.4	251	4	US-10-127-890-104	Sequence 104, App
15	1279	99.4	251	4	US-10-127-890-105	Sequence 105, App
16	1279	99.4	251	4	US-10-127-890-106	Sequence 106, App
17	1279	99.4	251	4	US-10-127-890-109	Sequence 109, App
18	1279	99.4	251	5	US-10-717-243-103	Sequence 103, App
19	1279	99.4	251	5	US-10-717-243-104	Sequence 104, App
20	1279	99.4	251	5	US-10-717-243-105	Sequence 105, App
21	1279	99.4	251	5	US-10-717-243-106	Sequence 106, App
22	1279	99.4	251	5	US-10-717-243-109	Sequence 109, App
23	1278	99.3	251	4	US-10-127-890-99	Sequence 99, Appl
24	1278	99.3	251	4	US-10-127-890-100	Sequence 100, App
25	1278	99.3	251	4	US-10-127-890-102	Sequence 102, App
26	1278	99.3	251	4	US-10-127-890-107	Sequence 107, App
27	1278	99.3	251	5	US-10-717-243-99	Sequence 99, Appl
28	1278	99.3	251	5	US-10-717-243-100	Sequence 100, App
29	1278	99.3	251	5	US-10-717-243-102	Sequence 102, App
30	1278	99.3	251	5	US-10-717-243-107	Sequence 107, App
31	1269	98.6	251	4	US-10-127-890-101	Sequence 101, App
32	1269	98.6	251	5	US-10-717-243-101	Sequence 101, App
33	1261	98.0	251	4	US-10-127-890-110	Sequence 110, App
34	1261	98.0	251	5	US-10-717-243-110	Sequence 110, App
35	1252	97.3	251	4	US-10-127-890-111	Sequence 111, App
36	1252	97.3	251	5	US-10-717-243-111	Sequence 111, App
37	1219.5	94.8	513	5	US-10-926-731A-12	Sequence 12, Appl
38	1208	93.9	506	5	US-10-964-195-11	Sequence 11, Appl
39	346	26.9	263	4	US-10-127-890-4	Sequence 4, Appli
40	346	26.9	263	5	US-10-717-243-4	Sequence 4, Appli
41	343	26.7	267	4	US-10-282-935-1	Sequence 1, Appli
42	343	26.7	267	4	US-10-127-890-1	Sequence 1, Appli
43	343	26.7	267	4	US-10-440-796-1	Sequence 1, Appli
44	343	26.7	267	5	US-10-717-243-1	Sequence 1, Appli
45	343	26.7	268	6	US-11-010-795-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1
 US-09-765-527-247
 ; Sequence 247, Application US/09765527
 ; Patent No. US20020006638A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
 ; Fusion Proteins and BPI-Derived Peptides
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/765,527
 ; FILING DATE: 18-Jan-2001
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/621,803
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Borun, Michael F.
 ; REGISTRATION NUMBER: 25,447
 ; REFERENCE/DOCKET NUMBER: 27129/33199
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/474-6300
 ; TELEFAX: 312/474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 247:
 ; SEQUENCE CHARACTERISTICS:

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; MOLÉCULE TYPE: protein
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
;
US-10-127-R90-2

RESULT 3

US-10-717-2

; Sequence 2, Application US/10717243
; Publication No. US20050054835A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
 Carroll, Stephen

Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

NUMBER OF SEQUENCES 100

NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

ZIP: 00001 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 1

FILING DATE: 18-Nov-2003

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION FORM

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 0

FILED DATE: 18-APR-
APPLICATION NUMBER:

APPLICATION NUMBER: 03-08/004,691
FILING DATE: 13-MAY-1993

FILED DATE: 12-MAY-1995
APPLICATION NUMBER: US 0

FILING NUMBER: 03-07-988,450
FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 0

FILING DATE: 19-JUN-1992

; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8889
 ; TELEFAX: 312/707-9155
 ; TELEX: 650 388-1248
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 251 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-717-243-2

Query Match 100.0%; Score 1287; DB 5; Length 251;
 Best Local Similarity 100.0%; Pred. No. 7e-117;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
 |||||||
 Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

 Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
 |||||||
 Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120

 Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
 |||||||
 Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

 Qy 181 FQQRIRPANNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
 |||||||
 Db 181 FQQRIRPANNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

 Qy 241 ALLKFVDKDPK 251
 |||||||||
 Db 241 ALLKFVDKDPK 251

RESULT 4
 US-10-074-596-1
 ; Sequence 1, Application US/10074596
 ; Publication No. US20030176331A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSENBLUM, MICHAEL G.
 ; APPLICANT: CHEUNG, LAWRENCE
 ; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
 ; TITLE OF INVENTION: MAKING THEEOF
 ; FILE REFERENCE: CLFR:007US
 ; CURRENT APPLICATION NUMBER: US/10/074,596
 ; CURRENT FILING DATE: 2002-02-12
 ; PRIOR APPLICATION NUMBER: 60/268,402
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 316
 ; TYPE: PRT
 ; ORGANISM: Gelonium multiflorum
 US-10-074-596-1

Query Match 100.0%; Score 1287; DB 4; Length 316;
 Best Local Similarity 100.0%; Pred. No. 9.6e-117;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
 |||||||
 Db 47 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 106

 Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
 |||||||

Db 107 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 166
Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
|||
Db 167 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 226
Qy 181 FQQRIRPANNNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
|||
Db 227 FQQRIRPANNNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 286
Qy 241 ALLKFVDKDPK 251
|||
Db 287 ALLKFVDKDPK 297

RESULT 5

US-10-964-195-13

; Sequence 13, Application US/10964195
; Publication No. US20050163774A1
; GENERAL INFORMATION:
; APPLICANT: Rosenblum et al.
; TITLE OF INVENTION: Immunotoxins Directed Against c-erbB-2 (HER-2/Neu)
; TITLE OF INVENTION: Related Surface Antigens
; FILE REFERENCE: D5425CIP2
; CURRENT APPLICATION NUMBER: US/10/964,195
; CURRENT FILING DATE: 2004-10-13
; PRIOR APPLICATION NUMBER: US/09/320,156
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 08/404,499
; PRIOR FILING DATE: 1995-03-17
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 13
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Polypeptide encoded by the scFv23-gelonin immunotoxin

US-10-964-195-13

Query Match 100.0%; Score 1287; DB 5; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.8e-116;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
|||
Db 247 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 306
Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
|||
Db 307 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 366
Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
|||
Db 367 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 426
Qy 181 FQQRIRPANNNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
|||
Db 427 FQQRIRPANNNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 486
Qy 241 ALLKFVDKDPK 251
|||
Db 487 ALLKFVDKDPK 497

RESULT 6

US-10-074-596-11

; Sequence 11, Application US/10074596
; Publication No. US20030176331A1
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MICHAEL G.
; APPLICANT: CHEUNG, LAWRENCE
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
; TITLE OF INVENTION: MAKING THEEOF
; FILE REFERENCE: CLFR:007US
; CURRENT APPLICATION NUMBER: US/10/074,596
; CURRENT FILING DATE: 2002-02-12

; PRIOR APPLICATION NUMBER: 60/268,402
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-074-596-11

Query Match 100.0%; Score 1287; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.8e-116;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHIGPLLRKKCDDPGKCFVLVALSNDN 60
Db 257 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHIGPLLRKKCDDPGKCFVLVALSNDN 316

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFHGGSYPSLEGEK 120
Db 317 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFHGGSYPSLEGEK 376

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 180
Db 377 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNN 436

Qy 181 FQQRIRPANNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 437 FQQRIRPANNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 496

Qy 241 ALLKFVDKDPK 251
Db 497 ALLKFVDKDPK 507

RESULT 7

US-09-765-527-259

; Sequence 259, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 259:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 259:
US-09-765-527-259

Query Match          99.8%; Score 1284; DB 3; Length 293;
Best Local Similarity 99.6%; Pred. No. 1.7e-116;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 82

Qy      61 GQIAEIAIDVTTSVYVVGVYQVRNRYSFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| :||| |
Db      83 GQIAEIAIDVTTSVYVVGVYQVRNRYSFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSEGEK 142

Qy      121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      143 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 202

Qy      181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      203 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 262

Qy      241 ALLKFVDKDPK 251
        ||||||| |||||
Db      263 ALLKFVDKDPK 273

```

RESULT 8
US-09-765-527-253
; Sequence 253, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 253:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 253:
US-09-765-527-253

Query Match 99.8%; Score 1284; DB 3; Length 309;
Best Local Similarity 99.6%; Pred. No. 1.8e-116;

Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
 |||||||
 Db 23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 82
 |||||||
 Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
 |||||||:|||||||
 Db 83 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSLEGEK 142
 |||||||:
 Qy 121 AYRETTDLGIEPLRIGIKKKLDENAIIDNYKPTEIASSLLVVIQMVSSEARFTFIENQIRNN 180
 |||||||:
 Db 143 AYRETTDLGIEPLRIGIKKKLDENAIIDNYKPTEIASSLLVVIQMVSSEARFTFIENQIRNN 202
 |||||||:
 Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 240
 |||||||:
 Db 203 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 262
 |||||||:
 Qy 241 ALLKFVDKDPK 251
 |||||||:
 Db 263 ALLKFVDKDPK 273

RESULT 9

US-09-765-527-251

; Sequence 251, Application US/09765527

; Patent No. US20020006638A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides .

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/621,803
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 251:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 332 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 251:

US-09-765-527-251

Query Match 99.8%; Score 1284; DB 3; Length 332;
 Best Local Similarity 99.6%; Pred. No. 2e-116;
 Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

|||

Db 23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 82

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

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Db      ||||||| 83 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTPSLEGEK 142
Qy      121 AYRETTDLGIEPLRIGIKKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db      143 AYRETTDLGIEPLRIGIKKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 202
Qy      181 FQQRIRPANNNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 240
Db      203 FQQRIRPANNNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 262
Qy      241 ALLKFVDKDPK 251
Db      263 ALLKFVDKDPK 273

```

RESULT 10

US-11-084-080-26
; Sequence 26, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORF, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-gelonin

US-11-084-080-26

```

Query Match          99.7%;  Score 1283;  DB 6;  Length 751;
Best Local Similarity 99.6%;  Pred. No. 7.8e-116;
Matches 250;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db      254 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 313
Qy      61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTPSLEGEK 120
Db      314 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTPSLEGEK 373
Qy      121 AYRETTDLGIEPLRIGIKKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db      374 AYRETTDLGIEPLRIGIKKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 433
Qy      181 FQQRIRPANNNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 240
Db      434 FQQRIRPANNNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 493
Qy      241 ALLKFVDKDPK 251
Db      494 ALLKFVDKDPK 504

```

RESULT 11

US-10-127-890-108
; Sequence 108, Application US/10127890

; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-127-890-108

Query Match 99.6%; Score 1282; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.1e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHIGPLLRKKCDDPGKCFVLVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHIGPLLRKKCDDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSSYFFKDAPDAAYEGLFKNTIKTRLHF GG SYP SLEGEK 120
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSSYFFKDAPDAAYEGLFKNTCKTRLHF GG SYP SLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMSEARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMSEARFTFIENQIRNN 180

Qy 181 FQQRIRPANN TISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANN TISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
|||||||

RESULT 12
US-10-717-243-108
; Sequence 108, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-717-243-108

Query Match 99.6%; Score 1282; DB 5; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.1e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGPILLRKKDPPGKCFVLVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGPILLRKKDPPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFEGGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVVVGQVRNRSYFFKDAPDAAYEGLFKNTCKTRLHFEGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNNTISLENKGWKL~~S~~FQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 FQQRIRPANNNTISLENKGWKL~~S~~FQIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
||| ||| |||
Db 241 ALLKFVDKDPK 251

RESULT 13
US-10-127-890-103
; Sequence 103, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-127-890-103

Db 61 GQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
Qy 121 AYRETTDLGIEPLRIGIKLKDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKLKDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
Qy 181 FQQRIRPANNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDCDPK 251

RESULT 14

US-10-127-890-104

; Sequence 104, Application US/10127890

; Publication No. US20030166196A1.

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; Carroll, Stephen F.

; Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins

; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

; STREET: 500 West Madison Street, 34th floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/127,890

; FILING DATE: 23-Apr-2002

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/646,360

; FILING DATE: 13-MAY-1996

; APPLICATION NUMBER: PCT/US94/05348

; FILING DATE: 12-MAY-1994

; APPLICATION NUMBER: US 08/064,691

; FILING DATE: 12-MAY-1993

; APPLICATION NUMBER: US 07/988,430

; FILING DATE: 09-DEC-1992

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: McNicholas, Janet M.

; REGISTRATION NUMBER: 32,918

; REFERENCE/DOCKET NUMBER: 200-70.P4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8889

; TELEFAX: 312/707-9155

; TELEX: 650 388-1248

; INFORMATION FOR SEQ ID NO: 104:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 251 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 104:

US-10-127-890-104

Query Match 99.4%; Score 1279; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 4.2e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHF GGSPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHF GGSPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMVS E A R F T F I E N Q I R N N 180
Db 121 AYRETTDLGIEPLRIGIKL DENAIDNYKPTEIASSLLVVIQMVS E A R F T F I E N Q I R N N 180

Qy 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 15

US-10-127-890-105

; Sequence 105, Application US/10127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins

; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248

; INFORMATION FOR SEQ ID NO: 105:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:

US-10-127-890-105

Query Match 99.4%; Score 1279; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 4.2e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60

Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
||||||||||||||||||||||||||||||||||||||||||||
Db 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180
||||||||||||||||||||||||||||||||||||||||
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMSEAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
||||||||||||||||||||||||||||||||||||||||
Db 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
|||||||||||
Db 241 ALLCFVDKDPK 251

Search completed: July 20, 2006, 09:43:17

Job time : 82.5055 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 2.rapbn.

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This page gives you Search Results detail for the Application 10717243 and Search Result us-10-717-243-2.rapbn.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:40:39 ; Search time 14.8192 Seconds
 (without alignments)
 976.754 Million cell updates/sec

Title: US-10-717-243-2
 Perfect score: 1287
 Sequence: 1 GLDTVSFSTKGATYITYVNF.....AVDQVKPKIALLKFVDKDPK 251

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 208217 seqs, 57668156 residues

Total number of hits satisfying chosen parameters: 208217

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_New:
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	343	26.7	267	7	US-11-263-537-1	Sequence 1, Appli
2	314	24.4	251	7	US-11-263-537-3	Sequence 3, Appli
3	124.5	9.7	282	6	US-10-449-902-56587	Sequence 56587, A
4	110.5	8.6	277	6	US-10-953-349-30545	Sequence 30545, A
5	110.5	8.6	277	7	US-11-056-355B-61236	Sequence 61236, A
6	110.5	8.6	281	6	US-10-953-349-30544	Sequence 30544, A
7	110.5	8.6	281	7	US-11-056-355B-61235	Sequence 61235, A
8	110.5	8.6	298	6	US-10-953-349-30543	Sequence 30543, A
9	110.5	8.6	298	7	US-11-056-355B-61234	Sequence 61234, A

10	108	8.4	298	6	US-10-449-902-39064	Sequence 39064, A
11	102.5	8.0	232	6	US-10-953-349-10528	Sequence 10528, A
12	102.5	8.0	245	6	US-10-953-349-10527	Sequence 10527, A
13	102.5	8.0	252	6	US-10-953-349-10526	Sequence 10526, A
14	91	7.1	876	6	US-10-471-571A-5500	Sequence 5500, Ap
15	88.5	6.9	239	6	US-10-953-349-14022	Sequence 14022, A
16	88.5	6.9	239	7	US-11-056-355B-55899	Sequence 55899, A
17	88.5	6.9	248	6	US-10-953-349-14021	Sequence 14021, A
18	88.5	6.9	248	7	US-11-056-355B-55898	Sequence 55898, A
19	88.5	6.9	254	6	US-10-953-349-14020	Sequence 14020, A
20	88.5	6.9	254	7	US-11-056-355B-55897	Sequence 55897, A
21	87	6.8	767	6	US-10-449-902-56749	Sequence 56749, A
22	86.5	6.7	296	6	US-10-449-902-41985	Sequence 41985, A
23	85	6.6	642	6	US-10-449-902-54461	Sequence 54461, A
24	82.5	6.4	278	7	US-11-056-355B-3125	Sequence 3125, Ap
25	82.5	6.4	342	6	US-10-471-571A-1372	Sequence 1372, Ap
26	82.5	6.4	388	6	US-10-953-349-20990	Sequence 20990, A
27	82.5	6.4	388	7	US-11-056-355B-53616	Sequence 53616, A
28	82.5	6.4	433	6	US-10-953-349-20989	Sequence 20989, A
29	82.5	6.4	433	7	US-11-056-355B-53615	Sequence 53615, A
30	82.5	6.4	450	6	US-10-953-349-20988	Sequence 20988, A
31	82.5	6.4	450	7	US-11-056-355B-53614	Sequence 53614, A
32	82.5	6.4	1183	6	US-10-471-571A-3398	Sequence 3398, Ap
33	82	6.4	291	6	US-10-449-902-37995	Sequence 37995, A
34	81.5	6.3	552	7	US-11-233-089-24	Sequence 24, Appl
35	81.5	6.3	763	6	US-10-449-902-43163	Sequence 43163, A
36	80.5	6.3	219	6	US-10-953-349-5981	Sequence 5981, Ap
37	80.5	6.3	219	7	US-11-056-355B-23415	Sequence 23415, A
38	80.5	6.3	219	7	US-11-056-355B-24652	Sequence 24652, A
39	80.5	6.3	219	7	US-11-056-355B-28637	Sequence 28637, A
40	80.5	6.3	219	7	US-11-056-355B-32227	Sequence 32227, A
41	80.5	6.3	219	7	US-11-056-355B-40030	Sequence 40030, A
42	80.5	6.3	219	7	US-11-056-355B-100712	Sequence 100712,
43	80.5	6.3	219	7	US-11-056-355B-111951	Sequence 111951,
44	80.5	6.3	260	6	US-10-953-349-5980	Sequence 5980, Ap
45	80.5	6.3	260	7	US-11-056-355B-23414	Sequence 23414, A

ALIGNMENTS

RESULT 1
US-11-263-537-1
; Sequence 1, Application US/11263537
; Publication No. US20060100135A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
; TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
; FILE REFERENCE: UTSD:884USC1
; CURRENT APPLICATION NUMBER: US/11/263,537
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: 10/282,935
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-263-537-1

Query Match 26.7%; Score 343; DB 7; Length 267;
Best Local Similarity 36.8%; Pred. No. 2.8e-23;
Matches 93; Conservative 45; Mismatches 99; Indels 16; Gaps 9;

Qy 5 VSFSTKGATYITYVNFLNELRVKLKPEGN-SHGIPLLRKKCDDP-GKCFVLVALSNDNGQ 62
 ::|:|| || :| :| :| :| :| :| :| :| :| :| :|
 Db 9 INFITAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINQRFLVELSNHAEL 68
 Qy 63 LAEIAIDVTSVYVVGYQVRNRSYFFKDAPD----AAYEGLFKNTIKTR--LHFGGSYPS 115
 :|:|||:| |||:| :| :| :| :| :| :| :| :| :|
 Db 69 SVTLALDVNTNAYVVGYRAGNSAYFFF--PDNQEDAEAITHLFTD-VQNRYTFAGGGNYDR 125
 Qy 116 LEGEKA-YRETTDLGIEPLRIGIKKLDENAINDKPTEIASSLLVVIQMSEAARFTFIE 174
 || :| :| :| :| :| :| :| :| :| :| :| :| :|
 bb 126 LEQLAGNLRENIELGNGLPEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 185
 Qy 175 NQIRN--NFQQRIRPANNNTISLENKWKGLSFQIRTSGANGMFSEAVELERANGKYYVTA 232
 ::| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 186 GEMRTRIRYNNRRSAPDPVSITLENSWGRNSTAIQESN-QGAFASPIQLQRRNGSKFSYD 244
 Qy 233 VDQVKPKIALLK 245
 | :| :| :|
 Db 245 VSILIPIALMVY 257

RESULT 2

US-11-263-537-3

; Sequence 3, Application US/11263537
 ; Publication No. US20060100135A1
 ; GENERAL INFORMATION:
 ; APPLICANT: VITETTA, ELLEN S.
 ; APPLICANT: GHETIE, VICTOR F.
 ; APPLICANT: SMALLSHAW, JOAN
 ; APPLICANT: BALUNA, ROXANA G.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
 ; TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
 ; FILE REFERENCE: UTSD:884USC1
 ; CURRENT APPLICATION NUMBER: US/11/263,537
 ; CURRENT FILING DATE: 2005-10-31
 ; PRIOR APPLICATION NUMBER: 10/282,935
 ; PRIOR FILING DATE: 2002-10-29
 ; PRIOR APPLICATION NUMBER: 09/538,873
 ; PRIOR FILING DATE: 2000-03-30
 ; PRIOR APPLICATION NUMBER: 60/126,826
 ; PRIOR FILING DATE: 1999-03-30
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 251
 ; TYPE: PRT
 ; ORGANISM: Abrus precatorius
 US-11-263-537-3

Query Match 24.4%; Score 314; DB 7; Length 251;
 Best Local Similarity 35.3%; Pred. No. 1e-20;
 Matches 90; Conservative 39; Mismatches 108; Indels 18; Gaps 8;
 Qy 5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKC----FVLVALSND 59
 :|:|||:| :| :| :| :| :| :| :| :| :| :| :|
 Db 5 IKFSTEGATSQSYKQFIEALRERLR-GGLIHDIPV---PDPTTLQERNRYITVELSNS 59
 Qy 60 NGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-G 118
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 60 DTESIEVGIDVTNAYVVAYRAGTQSFLRDAPSSASDYLFTGTDQHSLPFYGTGDLERW 119
 Qy 119 EKAYRETTDLGIEPLRIGIKKLDENAINDKPTEIASSLLVVIQMSEAARFTFIENQIR 178
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 120 AHQSRQQIPLGLQALTHGISFFRGNDN---EEKARTLIVIIQMVAARFRYISNRVR 176
 Qy 179 NNFQ--QRIRPANNNTISLENKWKGLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQ- 235
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 177 VSIFTGTAFQPDAAIMISLENNWDNLSRGVQES-VQDTFPNQVLTNIRNEPVIVDSLH 235
 Qy 236 VKPKIALLKFDKDP 250
 :|:|| :|
 Db 236 TVAVLALMLFVCNPP 250

RESULT 3

US-10-449-902-56587

; Sequence 56587, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56587
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-56587

RESULT 4

US-10-953-349-30545
; Sequence 30545, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30545
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30545

```

Query Match           8.6%; Score 110.5; DB 6; Length 277;
Best Local Similarity 21.9%; Pred. No. 0.021;
Matches 59; Conservative 49; Mismatches 116; Indels 45; Gaps 11;

Qy      2 LDTVSFSTKGATYITYVNFLNELRVKLK-PEGNSHGIPLLR--KKCDDPGKCFVLVALSN 58
       || |:: : |:  || |: : | ||: | :|| |: | : | : | :: :
Db      9 LFTATFNVQ-ASSTDYVTFITGIRNKLRLNPQGSSHHNRPVLPIEPNVPPSRWFHIVLKTS 67

Qy      59 DNGQLAELAIDVTSVYVGQVRNRSYFFKD---APDAAYEGLFKNTIKTRLHFGGSYPS 115

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; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30544
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30544

RESULT 7

US-11-056-355B-61235
; Sequence 61235, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fr.
; TITLE OF INVENTION: Polypeptides Encoded Ther.
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 61235
; LENGTH: 281
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(281)
; OTHER INFORMATION: Ceres Seq. ID no. 13661989
US-11-056-355B-61235

RESULT 10

US-10-449-902-39064

; Sequence 39064, A

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science

TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A020311-US
; CURRENT APPLICATION NUMBER: US

CURRENT AFFILIATION NUMBER: 03/107449,902
CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2001

PRIOR APPLICATION NUMBER: 31
PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-

; NUMBER OF SEQ

; SOFTWARE: Pa

; SEQ ID NO 39

; LENGTH: 298

; TYPE: PRT

Query Match 8.4%; Score 108; DB 0

Best Local Similarity 21.1%; Pred. No. 0.04; Matches 120; Signatures 41; Misses 100; Total 241; Score 1

Qy 21 LNELRVKLKPEGNSHGIPLLRKKCDD--PGKCFVLVALSNDNGQLAEIAIDVTSVYVVGVY 78
|| : || : || : || | : || | : || : || : || : || : || : || : || : || : || :
Ph 64 INTDRDVAGIREDPIL PVI ALDQWDPITVDPEDLILPKIYVANGCPTTILIPRDSHIVTEV 116

Qy 79 QVRNRSYF-FKDAPDAAYEGLFKNTIKTR-LHFGGSYPSLEGEKAYRETTDLGIEPLRIG 136
 : : | ||| : : | | || | : | : |
 Ph 139 ANVKGCGVEGSEVTPDPR LDESGERADLVEGEGVWMSLGRGSRVHILPQHEDRCEVMA 179

Qy 137 IKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNNFQQRIRPANNNTISLEN 196
 :| | : | : | ::::: || | | | : | : |
Pl 137 IKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNNFQQRIRPANNNTISLEN 196

Qy 197 KWGKLSFQIRTSGANG-----MFSEAVELERANGKKY 228
||:||: : | :| :|| :|

Page 11

RESULT 11

US-10-953-349-10528
SEARCHED - 10500 - 1 - 11/11/98 - US/10053348

Sequence 10528, Application US/

```
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 10528  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-10528
```

```

Query Match          8.0%; Score 102.5; DB 6; Length 232;
Best Local Similarity 23.5%; Pred. No. 0.088;
Matches 59; Conservative 36; Mismatches 95; Indels 61; Gaps 10;

Qy      17 YVNFLNELRVKLKPEGNSHGIPLLRKKCDPGKCFVL-----VALSNDNGQLAEIADV 70
        |::|: | : | : || | | | ::|| :| :| :| |
Db      7 YLFNFVQEAEQDNKKKNKEKDPL--KPKHPVSAFLVYANERRAALREENKSVVVA--- 60

Qy      71 TSVYVGVQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKAY----- 122
        : | : | : | | | : | : | : | | : | : | |
Db      61 ---KITGEEWKNLSS---DKKKAPYEVKVAKNKETYLQAMEEYKRTKEEEALSQKKEEEE 113

Qy      123 -----RETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEA 167
        : | | : : | : || : | : | : | : | |
Db      114 LLKLHKQEALQMLKKKEKTDNLNIKKEKATKKKNEN-VDPNKPKKPASSY----- 162

Qy      168 ARFTFIENQIRNNFQQQIRPANNTIS--LENKGWGLSFQIRT--SGANGMFSEAV--ELE 221
        | | ::| : | : | | : | : || : | : | | : | |
Db      163 --FLFSKDERKYLTEERPGTNATVTALISLKWKESEEKQVYNGKAALKMEAYKKEV 220

Qy      222 RANGKKYYVTA 232
        | | | : |
Db      221 AYNKKSAAATTS 231

```

RESULT 12

US-10-953-349-10527

```
; Sequence 10527, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10527
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10527
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Query Match           8.0%; Score 102.5; DB 6; Length 245;
Best Local Similarity 23.5%; Pred. No. 0.095;
Matches 59; Conservative 36; Mismatches 95; Indels 61; Gaps 10;

Qy      17 YVNFLNELRVKLKPEGNSHGIPLLRKKCDPGKCFVL-----VALSNDNGQLAEIAIDV 70
        ||::| | : | | : || | | | |::| || | : | : |:
Db      20 YLNFVQEAEQDNKKNNKKEKDPL---KPKHPVSASFIVYANERRAALREENKSVVEVA--- 73

Qy      71 TSVVVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEKAY----- 122
        : | : | | | | | || | : | | | | : |:
Db      74 ---KITGEEWKNLS---DKKKAPYEKVAKKNKETYLQAMEEYKRTKEEEALSQKKEEEE 126

Qy      123 -----RETTDLGIEPLRIGIKLKDENAIDNYKPTEIASSLLVVIQMSEA 167
        : | | | : | | : || | : | | | | | | |:
Db      127 LLKLHKQEALQMLKKKEKTDLNLIKKEKATKKKNEN-VDPNPKKKPASSY----- 175

Qy      168 ARFTIFIENQIRRNNOQIRPANNTIS--LENKGKLSFOIRT--SGANGMFSEAV--ELE 221

```

Db	176 --FLFSKDERKKLTERPGTNNATVTALISLKWKELSEEEKQVYNGKAAKLMEAYKKEVE 233
Qy	222 RANGKKYYVTA 232
Db	234 AYNKKSAATTS 244

RESULT 13

US-10-953-349-10526

; Sequence 10526, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINE
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10526
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10526

00 10 999 949 10526

Query Match 8.0%; Score 102.5; DB 6; Length 252;
Best Local Similarity 23.5%; Pred. No. 0.099;
Matches 59; Conservative 36; Mismatches 95; Indels 61; Gaps 10;

Qy 17 YVNFLNELRVKLKPEGNSHGPPLRKKCDPGKCFVL----VALSNDNGLAEIAIDV 70
 |:|- | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 27 YLNFVQEAEQDNKKNNKEKDPL--KPKHVPASFALVYANERRAALREENKSVVEVA-- 80

Qy	71 TSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKAY-----	122
Pb	81 ---KLTGEFHKNS---PKKKAKKKKAKKKKQETKLQMPREKQRTKTEFLGQKKEPEE-----	123

Qy 123 -----RETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLLVVIQMVS 167
: || : : || : || : || : ||

Qy 168 ARFTFIENQIRNNFQQIRPANNTIS--LENKGWKL SFQIRT--SGANGMFSEAV--ELE 221

Qy 222 RANGKKYYVTA 232

Db 241 AYNKKSAATTS 251

NSBBI-1
US-10-471

; Sequence 5500, Ap

; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,5
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 5500
; LENGTH: 876
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(876)
; OTHER INFORMATION: DNA polymerase I
US-10-471-571A-5500

Query Match 7.1%; Score 91; DB 6; Length 876;
 Best Local Similarity 19.6%; Pred. No. 5.6;
 Matches 52; Conservative 41; Mismatches 104; Indels 68; Gaps 9;

 Qy 37 IPLLKKCDDPGKCFVLVALSNDNGQLAELIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYE 96
 | | : | | | : :: | | :: | | : | : | | |
 Db 113 IGTLSKEADKAG--FQTIIITGDR-DLTQLATDNVTIYYTKKGVTDVDHYTPDFIAEKYN 169

 Qy 97 GLFKNTI-----KTRLHFGGSYPSLEGEKAYRETTDLGIEPLR 134
 || | | | | | : | : | : | : | : | : | : | : |
 Db 170 GLTPNQIIDMKGLMGDTSDNIPGVAVGVEKTAIKLLNQFDTVEGVYEHLD-----E 220

 Qy 135 IGIKKLDENAIDNYKPTEIASLKVQMVSEARFTFIENQIRNNFQQRIRPANN
 | | | | | : | | | : | | | : | | | | : |
 Db 221 ISGKKLKEK-LQNSKEDALMSKELATINVDSPIEVKLEDTLMTHQDEQQEKIELFKKLEF 279

 Qy 182 QQIRPANNTISLENKWGKLSFQIRTS-----GANGMFSEAVELER 222
 :| : | : | : | | : | | | | : | : | : | : |
 Db 280 KQLLADIDQSASVEDAIEK-TFEIETSFNDIDFTSLKEAAIHFELDGNNYLRRNILKFSL 338

 Qy 223 ANGKYYVTAVDQVKPKIALLKFVD 247
 | : | | | : | : | : | : | : | : |
 Db 339 FTGEKHIVINADDINNYVELVSWE 363

RESULT 15

US-10-953-349-14022
 ; Sequence 14022, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nickolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; TITLE OF INVENTION: ENCODED THERBY
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 14022
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 US-10-953-349-14022

Query Match 6.9%; Score 88.5; DB 6; Length 239;
 Best Local Similarity 22.9%; Pred. No. 1.7;
 Matches 47; Conservative 31; Mismatches 86; Indels 41; Gaps 8;

 Qy 51 FVLVAL---SNDNGQLAELIA---IDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKN-- 101
 |:::|| | | | | | : | : | : | | : | | | | |
 Db 7 FLILALAAGSSNQGGAAAAAGARPDLIVMKLHGHDPPEGPSVAFQ-THDLSFAG-FTNGG 64

 Qy 102 -----TIKTRLHFGGSYPSLEGEKAYRETTDLGIEPLRIGIKKLDENAIDNY 148
 | | | | | | | | | | | | | | | | | | | | |
 Db 65 GHWQAFPGLAHLFPPTSTPLPFGSSYDDLIGGLANLPRVPLGRQAMADAARVLSA---Y 119

 Qy 149 KPTEIAS-----SLLVVIQMVSSEARFTFIENQIRNNFQQRIRPANN
 | : | : | : | : | : | : | : | : | : | : |
 Db 120 DPSAAAADVEPVVKRALAALKVMLGDAQRLQPIHETVVRGWESESRVAPEHLPYIDHWDT 179

 Qy 201 LSFQI----RTSGANGMFSEAVELE 221
 :|::| | | | | | : | : |
 Db 180 ISYEIIRANRTGKWNGPFAKMLETQ 204

Search completed: July 20, 2006, 09:41:18
 Job time : 14.8192 secs

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 2.rup.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:36:29 ; Search time 257.947 Seconds
(without alignments)
900.105 Million cell updates/sec

Title: US-10-717-243-2
Perfect score: 1287
Sequence: 1 GLDTVSFSTKGATYITYVNF.....AVDQVKPKIALLKFVDKDPK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1287	100.0	316	1	RIPG_GELMU	P33186 gelonium mu
2	1242.5	96.5	258	2	Q9S9E4_GELMU	Q9s9e4 gelonium mu
3	394.5	30.7	581	2	Q94BW5_CINCA	Q94bw5 cinnamomum
4	393.5	30.6	580	2	Q94BW3_CINCA	Q94bw3 cinnamomum
5	392.5	30.5	549	2	Q9FV22_CINCA	Q9fv22 cinnamomum
6	388	30.1	299	2	Q8GZN9_9ROSI	Q8gzn9 euphorbia s
7	386.5	30.0	580	2	Q94BW4_CINCA	Q94bw4 cinnamomum
8	361.5	28.1	563	2	Q8GT32_SAMNI	Q8gt32 sambucus ni
9	357.5	27.8	297	2	Q8GZP0_9ROSI	Q8gzp0 euphorbia s
10	352	27.4	563	1	NIGB_SAMNI	P33183 sambucus ni
11	352	27.4	563	2	Q945S2_SAMNI	Q945s2 sambucus ni
12	348.5	27.1	563	2	O04367_SAMNI	O04367 sambucus ni
13	346	26.9	264	2	Q684J5_MOMCH	Q684j5 momordica c
14	346	26.9	286	1	RIP2_MOMBA	P29339 momordica b
15	346	26.9	286	1	RIP3_MOMCH	P24817 momordica c

16	346	26.9	286	2	Q5PZ05_MOMCH	Q5pz05 momordica c
17	344	26.7	541	2	Q41174_RICCO	Q41174 ricinus com
18	343	26.7	576	1	RICI_RICCO	P02879 ricinus com
19	341.5	26.5	265	1	RIP2_PHYDI	P34967 phytolacca
20	338.5	26.3	294	1	RIP1_TRIAN	P56626 trichosanth
21	337.5	26.2	564	2	Q9AVR2_9DIPS	Q9avr2 sambucus eb
22	334.5	26.0	564	1	AGGL_RICCO	P06750 ricinus com
23	333.5	25.9	527	1	ABRB_ABRPR	Q06077 abrus preca
24	333	25.9	282	1	RIP2_BRYDI	P98184 bryonia dio
25	330.5	25.7	294	1	RIPA_PHYAM	Q03464 phytolacca
26	329	25.6	252	2	Q38760_ABRPR	Q38760 abrus preca
27	327.5	25.4	293	2	Q8VYU0_9ROSI	Q8vyu0 jatropha cu
28	327.5	25.4	294	2	Q8H1W1_PHYAM	Q8h1w1 phytolacca
29	325.5	25.3	275	2	Q84LJ1_GYNPE	Q84lj1 gynostemma
30	325	25.3	313	1	RIP1_PHYAM	P10297 phytolacca
31	325	25.3	313	2	Q53YN2_PHYAM	Q53yn2 phytolacca
32	325	25.3	313	2	Q6PWU4_PHYAM	Q6pwu4 phytolacca
33	324.5	25.2	277	2	Q84JR1_GYNPE	Q84jr1 gynostemma
34	324.5	25.2	293	2	Q8S452_9ROSI	Q8s452 jatropha cu
35	324	25.2	289	2	Q41216_TRIKI	Q41216 trichosanth
36	323.5	25.1	277	2	Q8GV09_GYNPE	Q8gv09 gynostemma
37	322.5	25.1	275	2	Q8H1Y4_GYNPE	Q8h1y4 gynostemma
38	322.5	25.1	298	2	Q5FOI3_GYNPE	Q5f0i3 gynostemma
39	321	24.9	289	1	RIPT_TRIKI	P09989 trichosanth
40	321	24.9	289	2	Q94KE4_TRIKI	Q94ke4 trichosanth
41	321	24.9	567	2	Q6H267_VISAL	Q6h267 viscum albu
42	320.5	24.9	277	2	Q8GV11_GYNPE	Q8gv11 gynostemma
43	320.5	24.9	565	2	Q04071_SAMNI	Q04071 sambucus ni
44	320	24.9	251	2	Q7DM12_ABRPR	Q7dm12 abrus preca
45	320	24.9	252	2	Q38761_ABRPR	Q38761 abrus preca

ALIGNMENTS

RESULT 1
 RIPG_GELMU

ID RIPG_GELMU STANDARD; PRT; 316 AA.
 AC P33186;
 DT 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1995, sequence version 2.
 DT 07-FEB-2006, entry version 44.
 DE Ribosome-inactivating protein gelonin precursor (EC 3.2.2.22) (rRNA N-glycosidase).
 GN Name=GEL;
 OS *Gelonium multiflorum* (Euphorbiaceae himalaya).
 OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotoneoideae;
 OC Gelonieae; *Gelonium*.
 OC NCBI_TaxID=3979;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RX MEDLINE=94085781; PubMed=7916721; DOI=10.1016/0378-1119(93)90097-M;
 RA Nolan P.A., Garrison D.A., Better M.;
 RT "Cloning and expression of a gene encoding gelonin, a ribosome-inactivating protein from *Gelonium multiflorum*";
 RL Gene 134:223-227(1993).
 RN [2]
 RP PROTEIN SEQUENCE OF 47-93.
 RC TISSUE=Seed;
 RX MEDLINE=89326691; PubMed=2753596;
 RA Montecucchi P.-C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
 RA Lappi D.;
 RT "N-terminal sequence of some ribosome-inactivating proteins";
 RL Int. J. Pept. Protein Res. 33:263-267(1989).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RX MEDLINE=95333189; PubMed=7608981;
 RA Hosur M.V., Nair B., Satyamurthy P., Misquith S., Surolia A.,
 RA Kannan K.K.;
 RT "X-ray structure of gelonin at 1.8-A resolution";
 RL J. Mol. Biol. 250:368-380(1995).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SUBUNIT: Homodimer.

CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RIP subfamily.
 CC
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 CC
 DR EMBL; L12243; AAA16312.1; -; mRNA.
 DR PIR; JT0753; JT0753.
 DR HSSP; P09989; 1MRJ.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PRO0396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;
 KW Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 26 Potential.
 FT PROPEP 27 46
 FT CHAIN 47 297 Ribosome-inactivating protein gelonin.
 FT PROPEP 298 316 Removed in mature form.
 FT ACT_SITE 212 212
 FT CARBOHYD 235 235 N-linked (GlcNAc. .).
 FT DISULFID 90 96
 FT CONFLICT 90 90 C -> K (in Ref. 2).
 FT CONFLICT 93 93 P -> D (in Ref. 2).
 SQ SEQUENCE 316 AA; 35419 MW; 1252F3E710901B85 CRC64;

 Query Match 100.0%; Score 1287; DB 1; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.6e-101;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
 |||||||
 Db 47 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 106

 Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
 |||||||
 Db 107 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 166

 Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
 |||||||
 Db 167 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 226

 Qy 181 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMSEAVELERANGKYYVTAVDQVKPKI 240
 |||||||
 Db 227 FQQRIRPANNNTISLENKWGKLSFQIRTSGANGMSEAVELERANGKYYVTAVDQVKPKI 286

 Qy 241 ALLKFVDKDPK 251
 |||||||||
 Db 287 ALLKFVDKDPK 297

RESULT 2
 Q9S9E4_GELMU
 ID Q9S9E4_GELMU PRELIMINARY; PRT; 258 AA.
 AC Q9S9E4;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 21.
 DE rRNA -glycosidase (EC 3.2.2.22) (rRNA N-glycosidase).
 OS *Gelonium multiflorum* (Euphorbiaceae himalaya).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
 OC Gelonieae; *Gelonium*.
 OX NCBI_TaxID=3979;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=96006751; PubMed=7553224;
 RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,
 RA Toman P.D., Cheung L.;
 RT "Amino acid sequence analysis, gene construction, cloning, and
 RT expression of gelonin, a toxin derived from *Gelonium multiflorum*";
 RL J. Interferon Cytokine Res. 15:547-555(1995).

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 CC -----
 DR HSSP; P09989; 1MRJ.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
 SQ SEQUENCE 258 AA; 28826 MW; 13D68E673F4D6B06 CRC64;

Query Match 96.5%; Score 1242.5; DB 2; Length 258;
 Best Local Similarity 95.8%; Pred. No. 1.3e-97;
 Matches 248; Conservative 1; Mismatches 1; Indels 9; Gaps 2;

Qy	1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDPGKCFVLVALSNDN 60
Db	1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKG-DDPGKCFVLVALSNDN 59
Qy	61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTI-----KTRLHFGGS 112
Db	60 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKNPLLFGGKTRLHFGGS 119
Qy	113 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENADNYKPTEIASSLLVVIQMSEAARFTF 172
Db	120 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENADNYKPTEIASSLLVVIQMSEAARFTF 179
Qy	173 IENQIRNNFQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTA 232
Db	180 IENQIRNNFQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKYYVTA 239
Qy	233 VDQVKPKIALLKFDKDPK 251
	: :
Db	240 VDQVKPKIALLKFDKDPK 258

RESULT 3

Q94BW5_CINCA
 ID Q94BW5_CINCA PRELIMINARY; PRT; 581 AA.
 AC Q94BW5;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Type 2 ribosome-inactivating protein cinnamomin I precursor.
 OS Cinnamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
 OC Cinnamomum.
 OX NCBI_TaxID=13429;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
 RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
 RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated
 from the seeds of camphor tree and their expression patterns.";
 RL Gene 284:215-223(2002).

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 CC -----
 DR EMBL; AY039801; AAK82458.1; -; Genomic_DNA.
 DR HSSP; P02879; 2AAI.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 2.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.

DR PROSITE; PS50231; RICIN_B_LECTIN; 2.

KW Signal.

FT SIGNAL 1 32 Potential.

FT CHAIN 33 581 type 2 ribosome-inactivating protein cinnamomin I.

FT

SQ SEQUENCE 581 AA; 64216 MW; 6E8F5FB8FBA3D196 CRC64;

Query Match 30.7%; Score 394.5; DB 2; Length 581;
 Best Local Similarity 39.7%; Pred. No. 9.5e-25;
 Matches 100; Conservative 45; Mismatches 94; Indels 13; Gaps 8;

Qy	4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGPPLLRKKCDDP-GKCFVLVALSN--D 59
	:: : : : : ::: :
Db	35 TVTFTTKNATKTSYTQFIEALRAQLASGEEPHGIPVMRERSTVPDSKRFILVELSNWAAD 94
Qy	60 NGQLAEIFAIDVTSVYVVGYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSELEG 118
	: : : : : : : :
Db	95 SP--VTЛАVDVTNAYVVAYRTGSQSFFLREDNPDPAIENLLPDTKRYTFPFSGSYTDLEG 152
Qy	119 EKA-YRETTDLGIEPLRIGIKLKDENIAIDNYKPTEIASSLLVVIQMVESEAARFTFIENQI 177
	:: : : : : : ::
Db	153 VAGERREEILLGMDPLENAISALWISNLNQQR--ALARSLIVVIQMVAEAVRFRFIEYRV 210
Qy	178 RNNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYTAV-D 234
	: : : : : : : : .
Db	211 RGSISSRAEMFRPDPAMLSELENKWSALSNAVQQSNQGGVFSSPVELRSISNKPVYVGVSVD 270
Qy	235 QVKPKIALLKFV 246
	: : : :
Db	271 RVISGLAIMLFI 282

RESULT 4
Q94BW3_CINCA
ID Q94BW3_CINCA PRELIMINARY; PRT; 580 AA.
AC Q94BW3;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Type 2 ribosome-inactivating protein cinnamomin III precursor.
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated
from the seeds of camphor tree and their expression patterns.";
RL Gene 284:215-223(2002).
CC -----
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CC -----
DR EMBL; AY039803; AAK82460.1; -; Genomic_DNA.
DR HSSP; P02879; 2AAI.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
KW Signal.
FT SIGNAL 1 32 Potential.
FT CHAIN 33 580 type 2 ribosome-inactivating protein
cinnamomin III.
SQ SEQUENCE 580 AA; 64422 MW; 940D10F01E7FB558 CRC64;

Query Match 30.6%; Score 393.5; DB 2; Length 580;
Best Local Similarity 39.8%; Pred. No. 1.e-24;
Matches 101; Conservative 46; Mismatches 90; Indels 17; Gaps 9;

Qy 4 TVSFSTKGATYITYVNFLNELRVKKLPEGNSHGIPLLRKKCDDP-GKCFVLVALSN---D 59
 ||::|:|| || :| :|| :|| || ::||:||:| :|| |:|| || || |
 Db 35 TVTFTTKNATKTSYTQFIEALRAQLASGEYPHGPVMRERSTVPDSKRFILVELSNWAAD 94

 Qy 60 NGQLAEIAIDVTSVYVVGYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSLE- 117
 : :||:||: || |: :||:|| :|| || || |:|| :| || || ||
 Db 95 SP--VTLAVDVTNAYVVAERTGSQSSLREDNPDAIENLLPDTKRYTFPFSGSYTDLER 152

 Qy 118 --GEKAYRETTDLGIEPLRIGIKKLDENAINDNYPTEIASSLLVVIQMVAEARFTFIEN 175
 ||: || ||:|| | | :|| :|| :|| ||:||:|| || || || ||
 Db 153 VAGER--REEILLGMDPLENAISALWISNLNQQR--ALARSLIVVIQMVAEVRFRFIEY 208

 Qy 176 QIRNNF-QQRIRPANTTISLENKGWLKFQIRTSGANGMFSEAVELERANGKKYYVTAV 233
 ::| : :|| :|| || ::||:|| || :|| |:|| || || :|| || :|
 Db 209 RVRESITRAEMFRPDPAMLSLENKWSALSNAVQQSNQGGVFSSPVELRSISNKPVYVGTV 268

 Qy 234 -DQVKPKIALLKVF 246
 |:| :||:|:
 Db 269 SDRVVISGLAIMLFI 282

RESULT 5

Q9FV22_CINCA
 ID Q9FV22_CINCA PRELIMINARY; PRT; 549 AA.
 AC Q9FV22;
 DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2001, sequence version 1.
 DT 07-FEB-2006, entry version 19.
 DE Type II ribosome-inactivating protein cinnamomin (Fragment).
 OS Cinnamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
 OC Cinnamomum.
 OC NCBI_TaxID=13429;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Xie L., Liu W.-Y., Wang E.-D.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AF259548; AAF68978.2; -; mRNA.
 DR HSSP; P02879; 2AAI.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 2.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PRO0396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 FT NON_TER 1 1
 SQ SEQUENCE 549 AA; 60649 MW; 02607FE607CA44B0 CRC64;

Query Match 30.5%; Score 392.5; DB 2; Length 549;
 Best Local Similarity 39.7%; Pred. No. 1.3e-24;
 Matches 100; Conservative 45; Mismatches 94; Indels 13; Gaps 8;

Qy 4 TVSFSTKGATYITYVNFLNELRVKKLPEGNSHGIPLLRKKCDDP-GKCFVLVALSN---D 59
 ||::|:|| || :| :|| :|| || ::||:||:| :|| |:|| || || |
 Db 3 TVTFTTKNATKTSYTQFIEALRAQLASGEYPHGPVMRERSTVPDSKRFILVELSNWAAD 62

 Qy 60 NGQLAEIAIDVTSVYVVGYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSLEG 118
 : :||:||: || |: :||:|| :|| || || |:|| :| || || ||
 Db 63 SP--VTLAVDVTNAYVVAERTGSQSSLREDNPDAIENLLPDTKRYTFPFSGSYTDLEG 120

 Qy 119 EKA-YRETTDLGIEPLRIGIKKLDENAINDNYPTEIASSLLVVIQMVAEARFTFIENQI 177
 || |:|| | | | :|| :|| :|| ||:||:|| || || || :|
 Db 121 VAGERREEILLGMDPLENAISALWISNLNQQR--ALARSLIVVIQMVAEVRFRFIEYRV 178

 Qy 178 RNNFQ--QRIRPANTTISLENKGWLKFQIRTSGANGMFSEAVELERANGKKYYVTAV-D 234
 | : :|| :|| || ::|| || :|| |:|| || || :|| || :|
 Db 179 RGSISRAEMFRPDPAMLSLENKWSALSNAVQQSNQGGVFSSPVELRSISNKPVYVGTVSD 238

Qy 235 QVKPKIALLKFV 246
:| :|:: |:
Db 239 RVISGLAIMLFI 250

RESULT 6
Q8GNZ9_9ROSI
ID Q8GNZ9_9ROSI PRELIMINARY; PRT; 299 AA.
AC Q8GNZ9;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Ribosome inactivating protein Euserratin 2 precursor (EC 3.2.2.22).
GN Name=Eus2;
OS Euphorbia serrata.
OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Euphorbioideae;
OC Euphorbieae; Euphorbia.
OX NCBI_TaxID=196589;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Girbes T., Arias F.J., Benvenuto E.;
RT "Purification, characterization and molecular cloning of euserratins,
new type 1 ribosome-inactivating proteins from Euphorbia serrata L.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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CC
DR EMBL; AF457875; AAO15531.1; -; mRNA.
DR HSSP; Q9AVR2; 1HWN.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor;
KW Signal; Toxin.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 299 ribosome inactivating protein Euserratin
FT 2.
SQ SEQUENCE 299 AA; 33115 MW; DE791872B9CE2A7D CRC64;

Query Match 30.1%; Score 388; DB 2; Length 299;
Best Local Similarity 41.3%; Pred. No. 1.4e-24;
Matches 102; Conservative 36; Mismatches 97; Indels 12; Gaps 5;

Qy 4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKCD-DPGKCFVLVALSNDNGQ 62
:| :|: |: :| :|:: || :| || ||||| : ::|| || | :|
Db 30 SVKFTTHLASVGYSQSFMSLRKELDGSGSESHDIPLLRKPTEITNNNKYLLVNLINYDSQ 89

Qy 63 LA-EIAIDVTSVYVVGVYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEKA 121
|: :|: | :||:||: |:| |||| | ||: | | | | | |
Db 90 LSITLAVTVNVYVIGYKSAGNSFFLKDAPSDAKTLLFQGTNKITL--SSVDSNYNNLG 146

Qy 122 YRETTDLGIEPLRIGI---KKLDENAIIDNYKPTEIASLLVVIQMSEAARFTFIENQIR 178
| ||| || | | : ::| |||||||:||||| ||: :|
Db 147 DRSKVGLGIGPLSRSIDTLNKFNGVSNNV---FKESSLVVIQMVAEAARFKFQLKIE 202

Qy 179 NNFQQRIRPANNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKYYVTAVDQVQP 238
|| : | :||| || | || ||: || :| | : | || | :| |||
Db 203 NNLLDEYKPKNDTISYENNWEKLSEQIQLSGTDGKFKPVTLLYANGTDKIVSTVAQVQP 262

Qy 239 KIALLK 245
|::| :
Db 263 DISILLY 269

RESULT 7

Q94BW4_CINCA
ID Q94BW4_CINCA PRELIMINARY; PRT; 580 AA.
AC Q94BW4;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Type 2 ribosome-inactivating protein cinnamomin II precursor.
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated
from the seeds of camphor tree and their expression patterns.";
RL Gene 284:215-223(2002).
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CC -----
DR EMBL; AY039802; AAK82459.1; -; Genomic_DNA.
DR HSSP; P02879; 2AAI.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
KW Signal.
FT SIGNAL 1 32 Potential.
FT CHAIN 33 580 type 2 ribosome-inactivating protein
FT cinnamomin II.
SQ SEQUENCE 580 AA; 64266 MW; 37E4289ECCE0CBFF CRC64;

Query Match 30.0%; Score 386.5; DB 2; Length 580;
Best Local Similarity 39.8%; Pred. No. 4.5e-24;
Matches 101; Conservative 43; Mismatches 93; Indels 17; Gaps 9;

Qy 4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLRKKCDDP-GKCFVLVALSN---D 59
Db 35 TTVFTTKNATKTSYTQFIEALRAQLASGEEPHGIPVMDGSTVPSKRFILVELSNWAAD 94

Qy 60 NGQLAEIAIDVTSVYVGYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSLE- 117
Db 95 SP--VALAVDVTNAYVVAERTGSQFFLREDNPDPAIENLLPDTKRYTFPFSGSYTDLER 152

Qy 118 --GEKAYRETTDLGIEPLRIGIKKLDENAIKYKPTEIASSLLVIQMVEAARFTFIEN 175
Db 153 VAGE--LREEILLGMDPLENAISALWTSNLNQQR--ALARSLIVVIQMVAEAVRFRFIEY 208

Qy 176 QIRNNF--QQRIRPANNTISLENKGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAV 233
Db 209 RVRESITRAEMFRPDPAMLSENKWSALSNAVQQSNQGGVFSSPVELRSISNKPVYVGSV 268

Qy 234 -DQVKPKIALLKFV 246
Db 269 SDRVVISGLAIMLF 282

RESULT 8
Q8GT32_SAMNI
ID Q8GT32_SAMNI PRELIMINARY; PRT; 563 AA.
AC Q8GT32;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Type 2 ribosome-inactivating protein Nigrin 1 (EC 3.2.2.22).
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Girbes T., Arias F.J., Antolin P.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; AF249280; AAN86130.1; -; mRNA.
DR HSSP; Q9AVR2; 1HWM.
DR SMR; Q8GT32; 26-274, 299-560.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PRO0396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 563 AA; 62173 MW; OEB236421FC5E04F CRC64;

Query Match 28.1%; Score 361.5; DB 2; Length 563;
Best Local Similarity 41.0%; Pred. No. 6e-22;
Matches 94; Conservative 36; Mismatches 82; Indels 17; Gaps 8;

Qy 1 GLD--TVSFSTKGATYITYVNFLNELRVKLKPEG--NSHGIPLLRKKCDDPGKC-FVLVA 55
|:| :||: || || :|| | :||:||: : | |||
Db 25 GIDYPSVSFNLDGAKSATYRDFLSNLR-KTVATGYEVNGLPVLRRESEVQVKSRFVLVP 83

Qy 56 LSNDNGQLAEIAIDVTSVYVVGYQVRNRNSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPS 115
|:| || :||:||:|| : ||||||| : || | : || |:|| :|||
Db 84 LTNYNGNTVTLAVDVTNLYVVAFSGNANSYFFKDATEVQKSNLFVGTKQNTLSFTGNYDN 143

Qy 116 LE-GEKAYRETTDLGIEPLRIGIKKLDENADNYKPTEIASSLIVVIQMVSSEARFTFIE 174
|| || :|| || | | | | :| ||||||||||| :|||
Db 144 LETAAANTRRESIELGPSPLDGAITS-----YHGDSVARSLVVIQMVSSEARFRYIE 196

Qy 175 NQIRNNFQQ--RIRPANNTISLENKWKLSFQIRTSGAN-GMFSEAVEL 220
::|| :|| | : :||:|| | :|| :|| :|| | :|| | :|||
Db 197 QEVRRSLQQATSFTPNAWSLMSMENNWSMSLEIQQAGNNVSPFGTVQL 245

RESULT 9
Q8GZP0_9ROSI
ID Q8GZP0_9ROSI PRELIMINARY; PRT; 297 AA.
AC Q8GZP0;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Ribosome inactivating protein Euserratin 1 precursor (EC 3.2.2.22).
GN Name=Eus1;
OS Euphorbia serrata.
OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Euphorbioideae;
OC Euphorbieae; Euphorbia.
OX NCBI_TaxID=196589;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Girbes T., Arias F.J., Benvenuto E.;
RT "Purification, characterization and molecular cloning of euserratins,
RT new type 1 ribosome-inactivating proteins from Euphorbia serrata L.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; AF457874; AAO15530.1; -; mRNA.

DR HSSP; P33185; 1BRY.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor;
 KW Signal; Toxin.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 297 ribosome inactivating protein Euserratin
 FT 1.
 SQ SEQUENCE 297 AA; 33146 MW; A5269E1DDB91287A CRC64;

 Query Match 27.8%; Score 357.5; DB 2; Length 297;
 Best Local Similarity 39.8%; Pred. No. 5.7e-22;
 Matches 98; Conservative 39; Mismatches 98; Indels 11; Gaps 7;

 Qy 4 TVSFSTKGATYITYVNFLNELRVKLKGEGNSHGPILLRKKCD--DPGKCFVLVALSN-DN 60
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 29 TVKFTTHLASVGSYQTLMALSRVNLESKLESHNIPLLRKPSDITDQNK-YLLVELNYDT 87

 Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 88 KRTVTLALTIVLNVYVIGYKSGTKSFFLKDAPSDAKTLFTDTTPKTLEVDTNYNNL-GD- 145

 Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYK-PTEIASSLLVVIQMSEAARFTFIENQIRN 179
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 146 --RSKVGLGIPALKNAINIL--NQFDGVSTDQDFKHSLLIVIQMSEAARFKFIQLKIEG 201

 Qy 180 NFQQRIRPANNTISLENWKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPK 239
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 202 GLLTQYLPKPDTISYQNNWSALSKSIQLADANGRLSESVTLYEDGKDRVVFMVEQVQRD 261

 Qy 240 IALLKF 245
 :| :| :|
 Db 262 ISLLL 267

RESULT 10
 NIGB_SAMNI
 ID NIGB_SAMNI STANDARD PRT; 563 AA.
 AC P33183; P33184; P93542;
 DT 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.
 DT 05-DEC-2001, sequence version 2.
 DT 07-FEB-2006, entry version 56.
 DE Nigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chain
 (EC 3.2.2.22) (rRNA N-glycosidase); Nigrin b B chain].
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
 OX NCBI_TaxID=4202;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RC TISSUE=Bark;
 RX MEDLINE=96215449; PubMed=8647092;
 RA Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
 RT "Characterization and molecular cloning of Sambucus nigra agglutinin V
 (nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein
 from the bark of elderberry (Sambucus nigra).";
 RL Eur. J. Biochem. 237:505-513(1996).
 RN [2]
 RP PROTEIN SEQUENCE OF 26-49 AND 298-321.
 RC TISSUE=Bark;
 RX MEDLINE=94003077; PubMed=8400135;
 RA Girbes T., Cidores L., Ferreras J.M., Rojo M.A., Iglesias R.,
 RA Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;
 RT "Isolation and partial characterization of nigrin b, a non-toxic novel
 RT type 2 ribosome-inactivating protein from the bark of Sambucus nigra
 RT L.";
 RL Plant Mol. Biol. 22:1181-1186(1993).

CC -!- FUNCTION: Non-toxic type 2 RIP which strongly inhibits mammalian protein synthesis but does not affect plant nor bacterial protein synthesis. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal subunits by removing adenine from position 4,324 of 28S rRNA.
 CC -!- FUNCTION: The B chain is a galactose-specific lectin that facilitates the binding of nigrin b to the cell membrane that precedes endocytosis.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SUBUNIT: Disulfide-linked dimer of A and B chains.
 CC -!- SIMILARITY: In the N-terminal section; belongs to the ribosome-inactivating protein family. Type 2 RIP subfamily.
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC

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DR EMBL; U41299; AAB39475.1; -; mRNA.
 DR PIR; S37382; S37382.
 DR PIR; S37383; S37383.
 DR HSSP; Q9AVR2; 1HWM.
 DR SMR; P33183; 26-274, 299-560.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 2.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.

KW Direct protein sequencing; Glycoprotein; Hydrolase; Lectin;
 KW Plant defense; Protein synthesis inhibitor; Repeat; Signal; Toxin.

FT SIGNAL 1 25
 FT CHAIN 26 297 Nigrin b A chain.
 FT CHAIN 298 563 /FTId=PRO_0000030744.
 FT CHAIN 298 563 Nigrin b B chain.
 FT CHAIN 298 563 /FTId=PRO_0000030745.
 FT DOMAIN 305 431 Ricin B-type lectin 1.
 FT REPEAT 316 356 1-alpha.
 FT REPEAT 357 397 1-beta.
 FT REPEAT 400 432 1-gamma.
 FT DOMAIN 434 559 Ricin B-type lectin 2.
 FT REPEAT 445 482 2-alpha.
 FT REPEAT 486 524 2-beta.
 FT REPEAT 527 554 2-gamma.
 FT ACT_SITE 188 188 By similarity.
 FT CARBOHYD 221 221 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 368 368 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 376 376 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 483 483 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 537 537 N-linked (GlcNAc . .) (Potential).
 FT DISULFID 274 302 Interchain (between B and A chains) (By similarity).
 FT DISULFID 319 338 By similarity.
 FT DISULFID 360 377 By similarity.
 FT DISULFID 448 463 By similarity.
 FT DISULFID 489 506 By similarity.
 FT CONFLICT 39 39 K -> V (in Ref. 2).
 SQ SEQUENCE 563 AA; 62300 MW; F250CBE24621BF14 CRC64;

Query Match 27.4%; Score 352; DB 1; Length 563;
 Best Local Similarity 41.1%; Pred. No. 3.9e-21;
 Matches 90; Conservative 34; Mismatches 79; Indels 16; Gaps 7;

Qy 1 GLD--TWSFSTKGATIYTIVNFLNELRVVLKPEG--NSHGIPLRKKCDPGKC-FVLVA 55
 ||: :||: || || :||: || | :||:||: : | ||||
 Db 25 GIDYPSVSFNLDGAKSATYRDFLSNLR-KTVATGTYEVNGLPVLREREQVKSRFVLP 83
 Qy 56 LSNDNGQLAEIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPS 115
 ||: || || :||:||:|| : ||||||| : || | : || ||:||:
 Db 84 LTNYNGNTVTLAVDVTNLYVVAFSGNANSYFFKDATEVQKSNLFVGTKQNTLSFTGNYDN 143
 Qy 116 LE-GEKAYRETTDLGIEPLRIGIKKLDEAIDNYKPTEIASSLIVVIQMVSEAARFTFIE 174
 || ||: :|| || | | : || |||||||||||| :||
 Db 144 LETAANTRRESIELGPSPLDGAITSL-----YHGDSVARSLVVIQMVSEAARFRYIE 196

Qy 175 NQIRNNFQQ--RIRPANNNTISLENKWKLSFQIRTSGAN 211
 ::| : || | :||| | :| :| :| |
 Db 197 QEVRRSLQQATSFTPNALMSMENNWSSMSLEIQQAGNN 235

RESULT 11

Q945S2_SAMNI
 ID Q945S2_SAMNI PRELIMINARY; PRT; 563 AA.
 AC Q945S2;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Ribosome-inactivating protein.
 GN Name=AV1;
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
 OX NCBI_TaxID=4202;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Leaf;
 RA Van Damme E.J.M.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AF409135; AAL04123.1; -; mRNA.
 DR HSSP; Q9AVR2; 1HWM.
 DR SMR; Q945S2; 26-274, 299-560.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 2.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 SQ SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;

Query Match 27.4%; Score 352; DB 2; Length 563;
 Best Local Similarity 41.1%; Pred. No. 3.9e-21;
 Matches 90; Conservative 34; Mismatches 79; Indels 16; Gaps 7;

Qy 1 GLD--TWSFSTKGATYITYVNFLNELRVKLKPEG--NSHGIPLLRKKCDDPGKC-FVLVA 55
 ::| :|||: || || :||: || | :|||:|||: : | ||||
 Db 25 GIDYPSVSFNLDGAKSATYRDFLSNLR-KTVATGTYEVNGLPVLRRESEVQVKSRFVLP 83

Qy 56 LSNDNGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPS 115
 ::| || :|||:|||: || : | |||| | : || | : | | |:| :
 Db 84 LTNYNGNTVTLAVIDVTNLVYVAFSGNANSYFFKDATEVQKSNLVFGTKQNTLSFTGNYDN 143

Qy 116 LE-GEKAYRETTDLGIEPLRIGIKKLDEAIDNYKPTEIASSLIVVIQMVEAARFTFIE 174
 || ||:| :|| || | | | | :| |||||||:|||:||| :|||
 Db 144 LETAANTRRESIELGPSPLDGAITSL-----YHGDSVARSLLVVIQMVEAARFRYIE 196

Qy 175 NQIRNNFQQ--RIRPANNNTISLENKWKLSFQIRTSGAN 211
 ::| : || | :||| | :| :| :| |
 Db 197 QEVRRSLQQATSFTPNALMSMENNWSSMSLEIQQAGNN 235

RESULT 12

Q04367_SAMNI
 ID Q04367_SAMNI PRELIMINARY; PRT; 563 AA.
 AC Q04367;
 DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.
 DT 01-JUL-1997, sequence version 1.
 DT 07-FEB-2006, entry version 33.
 DE Ribosome inactivating protein precursor.
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98112023; PubMed=9450339;
RA Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
RA Peumans W.J.;
RT "The major elderberry (*Sambucus nigra*) fruit protein is a lectin
derived from a truncated type 2 ribosome-inactivating protein.";
RL Plant J. 12:1251-1260(1997).
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CC -----
DR EMBL; U76524; AAC15886.1; -; mRNA.
DR HSSP; Q9AVR2; 1HWM.
DR SMR; 004367; 26-276, 299-560.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPRO00772; Ricin_B_lectin.
DR InterPro; IPRO01574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 297 ribosome inactivating protein, A chain.
FT CHAIN 298 563 ribosome inactivating protein, B chain.
SQ SEQUENCE 563 AA; 62337 MW; 3ED2B6C08E796205 CRC64;

Query Match 27.1%; Score 348.5; DB 2; Length 563;
Best Local Similarity 39.7%; Pred. No. 7.7e-21;
Matches 91; Conservative 36; Mismatches 87; Indels 15; Gaps 7;

Qy 1 GLD--TWSFSTKGATYITYVNFLNELR-VKLKPEGNSHGIPLRKCKDDPGK-CFVLVAL 56
|:| :|||: || || :|| | : :||:||:: : | |||| |
Db 25 GIDYPSVSFNLAGAKSATYRDFLKNLRTIVATGTYEVNGLPVLRRESEVQVKNRFLVLL 84

Qy 57 SNONGQLAELIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSL 116
:| || :||:||:|| : | |||| | || | : | || |:| :|
Db 85 TNYNGNTVTLAVDVTNLYVVAFSANANSYFFKDATQLQKSNLFVGTRQHTLPFTGNYDNL 144

Qy 117 E-GEKAYRETTDLGIEPLRIGIKKKDENAIDNYKPTEIASSLLVIQMVSEAARFTFIEN 175
| :|| :|| || | | | : | :|| | | | | | :| :|| :||
Db 145 ETAAGTRRESIELGPSPLDGAITS-----YYDESVARSLLVIQMVSEAARFRYIEQ 197

Qy 176 QIRNNFQQR--IRPANNNTISLENKGWKLQFQIRTSGAN-GMFSEAVELE 221
:|| :| | :|| | :|| | :| ::| || | :| :||:
Db 198 EVRRSLQQTAGFTPNAIMLSMENNWWMSLEVQQSGDNVSPFTGTVQLQ 246

RESULT 13
Q684J5_MOMCH
ID Q684J5_MOMCH PRELIMINARY; PRT; 264 AA.
AC Q684J5;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Type I ribosome inactivating protein precursor (Fragment).
GN Name=rip;
OS Momordica charantia (Bitter gourd) (Balsam pear).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
OX NCBI_TaxID=3673;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HN1;
RA Nguyen Dinh C., Nguyen Thuy D., Le Thi Thu H., Nguyen Huy H.,
RA Tran Thi Phuong L., Nong Van H.;
RT "Expression of a gene encoding ribosome inactivating protein from
bitter melon (*Momordica charantia*).";
RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HN1;
 RA Nong V.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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 CC
 EMBL; AJ748278; CAH19208.1; -; Genomic_DNA.
 DR SMR; Q684J5; 2-264.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL <1 1 Potential.
 FT CHAIN 2 264 type I ribosome inactivating protein.
 FT NON_TER 1 1
 SQ SEQUENCE 264 AA; 29775 MW; AD9E1175B70521AD CRC64;

 Query Match 26.9%; Score 346; DB 2; Length 264;
 Best Local Similarity 37.4%; Pred. No. 4.7e-21;
 Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;

 Qy 5 VSFSTKGATYITYVNFLNELRVKKPENSHGIPPLRKCDPGKCFVLVALSNDNGQLA 64
 |:| || || |: :|| | : |||| | : ||: ||:: :
 Db 3 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISD-SRRFILLNLTSYAYETI 61

 Qy 65 EIAIDVTSVYVVGQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-GEKAYR 123
 :||||:|||| |: |: ||||:|| | || || | | : ||: ||: |
 Db 62 SVAIDVTNVYVVAYRTRDVSYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAHKIR 121

 Qy 124 ETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLIVVIQMVSEAARFTFIENQIRNNFQQ 183
 | ||: | | | : | !: ||:|| :||||:|| :||:
 Db 122 ENIDLGLPALSSAI----TTLFYNAQSAPSALLVLIQTTAEAARFKYIERHVAKYVAT 176

 Qy 184 RIRPANNTISLENKWKGKLSFQI-RTSGANGMFSEAVELERANGKKYYTAVDQ--VKPKI 240
 :| ||||:| || || | || | :||: | ::|| || || |
 Db 177 NFKNLAIISLENQWSALSKQIFLAQNQGGKFRNPVDLIKPTGERFQVTNVDSVVKGNI 236

 Qy 241 ALL 243
 |||
 Db 237 KLL 239

RESULT 14
 RIP2_MOMBA
 ID RIP2_MOMBA STANDARD; PRT; 286 AA.
 AC P29339;
 DT 01-DEC-1992, integrated into UniProtKB/Swiss-Prot.
 DT 01-DEC-1992, sequence version 1.
 DT 07-FEB-2006, entry version 40.
 DE Ribosome-inactivating protein momordin II precursor (EC 3.2.2.22)
 (rRNA N-glycosidase).
 OS Momordica balsamina (Bitter gourd) (Balsam apple).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
 OX NCBI_TaxID=3672;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC TISSUE=Seed;
 RX MEDLINE=93027170; PubMed=1408771;
 RA Ortigao M., Better M.;
 RT "Momordin II, a ribosome inactivating protein from Momordica
 balsamina, is homologous to other plant proteins.";
 RL Nucleic Acids Res. 20:4662-4662(1992).
 CC --!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC --!- SIMILARITY: Belongs to the ribosome-inactivating protein family.

CC Type 1 RIP subfamily.
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 CC
 DR EMBL; Z12175; CAA78166.1; -; Genomic_DNA.
 DR PIR; S25560; S25560.
 DR SMR; P29339; 24-286.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 23
 FT CHAIN 24 286 Ribosome-inactivating protein momordin
 II.
 FT /FTId=PRO_0000030772.
 FT ACT_SITE 181 181 By similarity.
 SQ SEQUENCE 286 AA; 32032 MW; 3B89FF1AE6B25986 CRC64;

 Query Match 26.9%; Score 346; DB 1; Length 286;
 Best Local Similarity 37.4%; Pred. No. 5.2e-21;
 Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;

 Qy 5 VSFSTKGATIYTVNLFNLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDNGQLA 64
 ||:|| || || :| :| | :|||| | :|:|:: :|:
 Db 25 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISD-SRRFILLDLTSYAYETI 83

 Qy 65 EIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-GEKAYR 123
 :||||:|||| |:|:||||:| || ||| | | :|:| :|:
 Db 84 SVAIDVTNVYVWAYRTRDVSYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAAHKIR 143

 Qy 124 ETTDLGIEPLRIGIKKLDEAIDNYKPTEIASSLIVIQMVSSEARFTFIENQIRNNFQQ 183
 | |||:| | | :| | :||||:|| :|||| :|||:
 Db 144 ENIDLGLPALSSAI----TTLFYNAQSAPSALLVLIQTTAEAAARFKYIERHVAKYVAT 198

 Qy 184 RIRPANNNTISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYVTAVDQ--VKPKI 240
 :| |||||:| || || | | | :|:| :|::| ||| || |
 Db 199 NFKNLAIISLENQWSALSKQIFLAQNQGGKFRNPVDLIKPTGERFQVTNVDSVVKGNI 258

 Qy 241 ALL 243
 ||
 Db 259 KLL 261

RESULT 15
 RIP3_MOMCH
 ID RIP3_MOMCH STANDARD; PRT; 286 AA.
 AC P24817; Q41257; Q9FSH2; Q9FUV7;
 DT 01-MAR-1992, integrated into UniProtKB/Swiss-Prot.
 DT 26-APR-2004, sequence version 2.
 DT 07-FEB-2006, entry version 46.
 DE Ribosome-inactivating protein beta-momorcharin precursor (EC 3.2.2.22)
 DE (rRNA N-glycosidase) (MAP 30) (B-MMC).
 GN Name=MAP30; Synonyms=RIP;
 OS Momordica charantia (Bitter gourd) (Balsam pear).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
 OX NCBI_TaxID=3673;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Leaf;
 RX MEDLINE=95394347; PubMed=7665070; DOI=10.1016/0378-1119(95)00186-A;
 RA Lee-Huang S., Huang P.L., Chen H.-C., Huang P.L., Bourinbaiar A.,
 RA Huang H.I., Kung H.-F.;
 RT "Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter
 melon.";
 RL Gene 161:151-156(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Quanhong Y., Rihe P., Aisheng X.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 23-286.
 RA Wei Y.-F., Cai L.-B., Zhuang W.;

RT "Cloning rip gene and identification of its resistance to Aspergillus
 RT flavus.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 23-286.
 RA Nguyen Huy H., Nghiem Ngoc M., Dao Huy P., Le Tran B., Nong Van H.;
 RT "Expression of a RIP gene from Momordica charantia in E. coli.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP PROTEIN SEQUENCE OF 24-67.
 RC TISSUE=Seed;
 RX MEDLINE=91032105; PubMed=1699801; DOI=10.1016/0014-5793(90)80438-O;
 RA Lee-Huang S., Huang P.L., Nara P.L., Chen H.-C., Kung H.-F., Huang P.,
 RA Huang H.I., Huang P.L.;
 RT "MAP 30: a new inhibitor of HIV-1 infection and replication.";
 RL FEBS Lett. 272:12-18(1990).
 RN [6]
 RP STRUCTURE BY NMR OF 24-286, AND DNA-BINDING.
 RX PubMed=10571185; DOI=10.1016/S0092-8674(00)81529-9;
 RA Wang Y.-X., Neamati N., Jacob J., Palmer I., Stahl S.J., Kaufman J.D.,
 RA Huang P.L., Huang P.L., Winslow H.E., Pommier Y., Wingfield P.T.,
 RA Lee-Huang S., Bax A., Torchia D.A.;
 RT "Solution structure of anti-HIV-1 and anti-tumor protein MAP30:
 RT structural insights into its multiple functions.";
 RL Cell 99:433-442(1999).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 24-272.
 RX PubMed=10329776; DOI=10.1107/S0907444999003297;
 RA Yuan Y.-R., He Y.-N., Xiong J.-P., Xia Z.-X.;
 RT "Three-dimensional structure of beta-momorcharin at 2.55 Å
 RT resolution.";
 RL Acta Crystallogr. D 55:1144-1151(1999).
 CC -!- FUNCTION: Irreversibly relaxes supercoiled DNA and catalyzes
 CC double-stranded breakage. Acts also as a ribosome inactivating
 CC protein.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- PTM: Bound to a branched hexasaccharide.
 CC -!- MISCELLANEOUS: Possesses anti-HIV and antitumoral activities.
 CC Inhibits HIV-1 integrase.
 CC -!- MISCELLANEOUS: Manganese or zinc required for enhancing substrate
 CC binding rather than catalysis.
 CC -!- MISCELLANEOUS: The oligosaccharide does not influence the fold of
 CC the polypeptide chain and probably does not play a role in the
 CC enzymatic function.
 CC -!- MISCELLANEOUS: Is not toxic to uninfected normal cells as it
 CC cannot enter into them.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RIP subfamily.
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 CC -----
 DR EMBL; S79450; AAB35194.2; -; Genomic_DNA.
 DR EMBL; AF284811; AAG33028.1; -; Genomic_DNA.
 DR EMBL; AY523412; AAS17014.1; -; mRNA.
 DR EMBL; AJ294541; CAC08217.1; -; Genomic_DNA.
 DR PIR; B61318; B61318.
 DR PIR; JC4235; JC4235.
 DR PDB; 1CF5; X-ray; A/B=24-272.
 DR PDB; 1D8V; NMR; A=24-286.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW 3D-structure; Antiviral protein; Direct protein sequencing;
 KW Glycoprotein; Hydrolase; Plant defense; Protein synthesis inhibitor;
 KW Signal; Toxin.
 FT SIGNAL 1 23
 FT CHAIN 24 286 Ribosome-inactivating protein beta-
 FT momorcharin.
 FT /FTId=PRO_0000030773.
 FT ACT_SITE 93 93 By similarity.
 FT ACT_SITE 132 132 By similarity.
 FT ACT_SITE 181 181 By similarity.
 FT ACT_SITE 184 184 By similarity.

FT	CARBOHYD	74	74	N-linked (GlcNAc. . .).
FT	CONFLICT	23	23	G -> M (in Ref. 3 and 4).
FT	CONFLICT	37	37	Y -> T (in Ref. 5).
FT	CONFLICT	67	67	S -> P (in Ref. 5).
FT	CONFLICT	147	147	D -> E (in Ref. 4).
FT	CONFLICT	188	188	I -> T (in Ref. 1).
FT	CONFLICT	228	228	G -> A (in Ref. 4).
FT	STRAND	25	28	
FT	HELIX	29	31	
FT	HELIX	34	45	
FT	TURN	46	47	
FT	STRAND	48	48	
FT	STRAND	50	54	
FT	TURN	55	56	
FT	STRAND	57	60	
FT	STRAND	62	63	
FT	TURN	66	67	
FT	STRAND	68	76	
FT	TURN	78	79	
FT	STRAND	82	88	
FT	TURN	89	91	
FT	STRAND	94	99	
FT	TURN	100	101	
FT	STRAND	102	106	
FT	TURN	107	108	
FT	HELIX	111	116	
FT	STRAND	117	118	
FT	TURN	119	120	
FT	STRAND	121	128	
FT	STRAND	130	131	
FT	HELIX	132	139	
FT	TURN	140	140	
FT	STRAND	141	141	
FT	HELIX	143	145	
FT	STRAND	146	146	
FT	STRAND	148	149	
FT	HELIX	150	161	
FT	TURN	162	162	
FT	TURN	165	167	
FT	HELIX	168	177	
FT	TURN	178	179	
FT	HELIX	180	184	
FT	STRAND	185	185	
FT	HELIX	186	194	
FT	STRAND	196	200	
FT	STRAND	204	204	
FT	HELIX	205	210	
FT	TURN	211	214	
FT	HELIX	215	222	
FT	TURN	223	228	
FT	STRAND	229	237	
FT	TURN	239	240	
FT	STRAND	241	241	
FT	STRAND	243	248	
FT	TURN	249	250	
FT	STRAND	251	251	
FT	HELIX	252	256	
FT	TURN	257	257	
FT	STRAND	258	258	
FT	STRAND	261	261	
FT	HELIX	264	269	
FT	TURN	270	271	
FT	TURN	274	276	
FT	TURN	279	281	
FT	STRAND	282	283	
SQ	SEQUENCE	286 AA;	32031 MW;	6B2DF55A41D8F921 CRC64;

Query Match 26.9%; Score 346; DB 1; Length 286;
 Best Local Similarity 37.4%; Pred. No. 5.2e-21;
 Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;

Qy	5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLKKCDDPGKCFVLVALSNDNGQLA 64
	: : : : : : : : :: :
Db	25 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISD-SRRFILLNLTSYAYETI 83
Qy	65 EIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-GEKAYR 123

:|||||:|||| |: ||: |||||::| || |||| | | : ||| ::|
Db 84 SVAIDVTNVYVVAYRTRDVSYFFKESPPEAYNILFKGTRKITLPYTGNENLQTAHKIR 143
Qy 124 ETTDLGIEPLRIGIKKLDENAIIDNYKPTEIASSLLVVIQMVSEARFTFIENQIRNNFQQ 183
| |||: | | | : | | :|||:|| :||||| :|| |:
Db 144 ENIDLGLPALSSAI----TTLFYNAQSAPSALLVLIQTTAEAAARFKYIERHVAKYVAT 198
Qy 184 RIRPANNТИSLENKGKLSFQI-RTSGANGMFSEAVELERANGKKYYVTAVDQ--VKPKI 240
:| |||||:| || || | | | | :| :|::| || | | | |:
Db 199 NFKPNLAIISLENQWSALSKQIFLAQNQGGKFRNPVDLIKPTGERFQVTNVDSDVVKGNI 258
Qy 241 ALL 243
| |
Db 259 KLL 261

Search completed: July 20, 2006, 09:53:05
Job time : 261.197 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 56.rag.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10717243 and Search Result us-10-717-243-56.rag.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:35:59 ; Search time 16.1993 Seconds
(without alignments)
564.490 Million cell updates/sec

Title: US-10-717-243-56
Perfect score: 114
Sequence: 1 CHHHASRVARMASDEFPSMC 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:
9: geneseqp2005s:
10: geneseqp2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	114	100.0	20	2	AAR37300	Aar37300 E.coli sh
2	114	100.0	293	2	AAW58827	Aaw58827 Shiga tox
3	114	100.0	293	2	AAY39393	Aay39393 Shiga-lik
4	114	100.0	293	3	AAY69046	Aay69046 Amino aci
5	114	100.0	299	9	AED14646	Aed14646 Protein s
6	114	100.0	315	2	AAW06403	Aaw06403 Verotoxig
7	114	100.0	315	2	AAW21702	Aaw21702 Shiga-lik

8	114	100.0	315	2	AAW25139	Aaw25139 SLT-1 (a
9	114	100.0	315	3	AAY96681	Aay96681 E. coli v
10	114	100.0	315	5	AAU77817	Aau77817 E. coli v
11	114	100.0	315	7	ADC00545	Adc00545 Enterohae
12	114	100.0	315	7	ADH34319	Adh34319 Verotoxin
13	114	100.0	315	10	AEF18888	Aef18888 Shiga tox
14	114	100.0	316	2	AAW25786	Aaw25786 Phage H19
15	114	100.0	323	2	AAW06407	Aaw06407 Histidine
16	114	100.0	323	3	AAY96686	Aay96686 Recombina
17	114	100.0	323	5	AAU77822	Aau77822 HIS-tagge
18	114	100.0	326	2	AAW06413	Aaw06413 Flag tag/
19	114	100.0	326	3	AAY96692	Aay96692 FLAG tag-
20	114	100.0	326	5	AAU77828	Aau77828 Flag tag/
21	114	100.0	332	2	AAW29294	Aaw29294 BPI pepti
22	114	100.0	409	2	AAR13118	Aar13118 Shiga-lik
23	114	100.0	409	2	AAY55891	Aay55891 E.coli ba
24	114	100.0	409	3	AAY78591	Aay78591 E. coli b
25	114	100.0	690	3	AAY96694	Aay96694 MBP-VT-1
26	114	100.0	690	5	AAU77830	Aau77830 MBPNVT1-A
27	114	100.0	708	2	AAW06411	Aaw06411 Maltose b
28	114	100.0	708	3	AAY96690	Aay96690 MBP-VT-1
29	114	100.0	708	5	AAU77826	Aau77826 MBPNVT1-A
30	100.5	88.2	27	9	AED14669	Aed14669 MUC1 epit
31	100.5	88.2	27	9	AED14671	Aed14671 MUC1 epit
32	100.5	88.2	27	9	AED14665	Aed14665 MUC1 epit
33	100.5	88.2	27	9	AED14668	Aed14668 MUC1 epit
34	100.5	88.2	27	9	AED14672	Aed14672 MUC1 epit
35	100.5	88.2	27	9	AED14673	Aed14673 MUC1 epit
36	100.5	88.2	27	9	AED14666	Aed14666 MUC1 epit
37	100.5	88.2	27	9	AED14670	Aed14670 MUC1 epit
38	100.5	88.2	27	9	AED14664	Aed14664 Peptide s
39	100.5	88.2	27	9	AED14667	Aed14667 MUC1 epit
40	100.5	88.2	27	9	AED14674	Aed14674 MUC1 epit
41	100.5	88.2	302	9	AED14649	Aed14649 Shiga lik
42	100.5	88.2	319	9	AED14650	Aed14650 Shiga lik
43	51	44.7	17	9	ADZ89477	Adz89477 Substrate
44	47	41.2	135	7	ADJ68214	Adj68214 Human hea
45	46	40.4	18	9	ADZ89463	Adz89463 Substrate

ALIGNMENTS

RESULT 1
AAR37300
ID AAR37300 standard; protein; 20 AA.
XX
AC AAR37300;
XX
DT 25-MAR-2003 (revised)
DT 13-SEP-1993 (first entry)
XX
DE E.coli shiga-like toxin segment.
XX
KW Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;
KW autoimmune disease; cell killing; toxin; human engineered antibody;
KW variable region; light chain; cell targetting; chimeric antibody; SLT.
XX
OS Escherichia coli.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..20
FT /note= "intervening loop includes protease sensitive
FT amino acid sequence"
XX
PN WO9309130-A1.
XX
PD 13-MAY-1993.
XX
PF 04-NOV-1992; 92WO-US009487.
XX
PR 04-NOV-1991; 91US-00787567.
PR 19-JUN-1992; 92US-00901707.
XX
PA (XOMA) XOMA CORP.
XX

PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;
XX
DR WPI; 1993-167617/20.
XX
PT Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo.
XX
PS Example 10; Page 114; 163pp; English.
XX
CC The invention covers analogues of the plant type I RIP gelonin which have a non-naturally occurring Cys residue in a position which enables the analogue to be conjugated via a disulphide linkage to a molecule which specifically binds to a target cell. Pref. target-cell binding molecules are antibodies or their fragments, esp. human engineered H65 antibody fragments. Fusion constructs were assembled that included a natural sequence gelonin gene fused to an H65 truncated heavy chain gene or an H65 light chain (kappa) gene. A DNA linker encoding a peptide segment of the E.coli shiga-like toxin was inserted between the gelonin gene and the Ab gene. The resulting immunoconjugates can be used as cytotoxic therapeutic agents. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.7e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
||| ||| ||| ||| ||| ||| ||| |||
Db 1 CHHHASRVARMASDEFPSMC 20

RESULT 2
AAW58827
ID AAW58827 standard; peptide; 293 AA.
XX
AC AAW58827;
XX
DT 18-AUG-1998 (first entry)
XX
DE Shiga toxin type 1 mature A subunit.
XX
KW Histine-tag; toxoid; antibody; treatment; diagnosis; prevention; Stx;
KW haemorrhagic colitis; haemolytic uremic syndrome.
XX
OS Shigella dysenteriae.
XX
PN WO9811229-A2.
XX
PD 19-MAR-1998.
XX
PF 09-SEP-1997; 97WO-US015836.
XX
PR 10-SEP-1996; 96US-0025637P.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI Obrien AD, Schmitt CK;
XX
DR WPI; 1998-207390/18.
DR N-PSDB; AAV11400.
XX
PT Purification and isolation of histidine-tagged Shiga toxins - useful in vaccines against haemorrhagic colitis and haemolytic uremic syndrome.
XX
PS Claim 1; Fig 2; 47pp; English.
XX
CC The Shiga toxin (Stx) peptides (AAW58827-W58830) were histidine-tagged to simplify and expedite purification. Non toxic Shiga toxoids, Fusion proteins of His-tagged Shiga toxins/toxoids and antibodies can be used in the treatment, diagnosis or prevention of infections mediated by toxins of the Stx family. These are associated with haemorrhagic colitis and the life-threatening sequela, haemolytic uremic syndrome. Shiga antibodies are also useful for the treatment, diagnosis and prevention of disease and infections by pathogenic Escherichia coli

XX
SQ Sequence 293 AA;

Query Match 100.0%; Score 114; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
|||||||||||||||||||
Db 242 CHHHASRVARMASDEFFPSMC 261

RESULT 3
AAV39393
ID AAV39393 standard; protein; 293 AA.

XX AC AAV39393;

XX DT 20-DEC-1999 (first entry)

XX DE Shiga-like Toxin 1, A subunit.

XX KW Shiga toxin; ShT; Shiga-like toxin; SLT; A subunit; B subunit; ricin;
KW microorganism clone; combinatorial library; therapeutic protein;
KW medicament; target cell; binding specificity.

XX OS Shigella dysenteriae.

XX PN WO9940185-A1.

XX PD 12-AUG-1999.

XX PF 08-DEC-1998; 98WO-CA001137.

XX PR 04-FEB-1998; 98CA-02222993.

XX PA (ONTA-) ONTARIO CANCER INST.

XX PI Gariepy J, Bray MR;

XX DR WPI; 1999-590695/50.

XX PT Production of cytotoxic heteromeric protein combinatorial libraries,
PT useful for ability to specifically bind to and kill a target cell.
XX PS Example 1; Fig 1a; 61pp; English.

CC This is the Shiga-like toxin (SLT) subunit A amino acid sequence. SLT is
CC a bacterial toxin related to the Shiga toxin (ShT). SLT and ShT have the
CC smallest known B subunit of all AB toxins, and the A subunit has
CC identical catalytic activity as the corresponding subunit in ricin. The B
CC subunit (AAV39394) is identical for both ShT and SLT. Both the A and B
CC subunit amino acid sequences are used in the methods of the invention,
CC which relates to the creation of a library of microorganism clones
CC producing mutant proteins which are then screened for their ability to
CC specifically bind to and kill target cell. AAV39395-Y39389 and AAV43001-
CC Y43024 are examples of mutant B subunits identified by the methods of the
CC invention. The B subunit of the toxin has high binding specificity, and
CC therefore mutant versions of the B subunit may target the toxin to a
CC specific cell. Cytotoxic mutant proteins identified by the method can be
CC used to identify therapeutic proteins and medicaments having binding
CC specificity for a target cell. The cytotoxic mutants can also be used to
CC construct diagnostic probes for detecting the presence of cell surface
CC markers. These medicaments can be used to target medicines to target
CC cells in host organisms

XX SQ Sequence 293 AA;

Query Match 100.0%; Score 114; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
|||||||||||||||
Db 242 CHHHASRVARMASDEFFPSMC 261

RESULT 4
AY69046
ID AY69046 standard; protein; 293 AA.
XX
AC AY69046;
XX
DT 30-MAY-2000 (first entry)
XX
DE Amino acid sequence of exemplary cell toxin shiga toxin A-chain.
XX
KW Chemokine receptor; ligand; inflammatory response; immune effector cell;
KW secondary tissue damage; central nervous system injury; shiga;
KW CNS inflammatory disease; neurodegenerative disorder; heart disease;
KW inflammatory eye disease; inflammatory bowel disease; PCR primer;
KW inflammatory joint disease; inflammatory kidney; renal disease;
KW inflammatory lung disease; inflammatory nasal disease; thyroiditis;
KW inflammatory thyroid disease; cytokine-regulated cancer; ss.
XX
OS Shigella dysenteriae.
XX
PN WO200004926-A2.
XX
PD 03-FEB-2000.
XX
PF 21-JUL-1999; 99WO-CA000659.
XX
PR 22-JUL-1998; 98US-00120523.
XX
PA (OSPR-) OSPREY PHARM LTD.
XX
PI Mcdonald JR, Coggins PJ;
XX
DR WPI; 2000-182542/16.
XX
PT A new therapeutic agent comprising a conjugate for treating secondary
PT tissue damage and other disease conditions like Alzheimer's disease,
PT stroke, Parkinson's disease and atherosclerosis.
XX
PS Disclosure; Page 67; 204pp; English.
XX
CC The present sequence represents an exemplary cell toxin, which can be
CC incorporated into the conjugates of the invention. The specification
CC describes a conjugate, comprising a targeted agent and a chemokine
CC receptor ligand. The conjugate binds to a chemokine receptor resulting in
CC internalisation of the targeted agent in cells bearing the receptor. The
CC conjugates are used for formulating a medicament or for treating
CC disorders associated with inflammatory responses resulting from
CC activation, proliferation and migration of immune effector cells. The
CC disorders or disease states comprise secondary tissue damage such as
CC central nervous system (CNS) injury, CNS inflammatory diseases,
CC neurodegenerative disorders, heart disease, inflammatory eye diseases,
CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory
CC kidney or renal diseases, inflammatory lung diseases, inflammatory nasal
CC diseases, inflammatory thyroid disease such as thyroiditis, or cytokine-
CC regulated cancers
XX
SQ Sequence 293 AA;

Query Match 100.0%; Score 114; DB 3; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
|||
Db 242 CHHHASRVARMASDEFPSMC 261

RESULT 5
AED14646
ID AED14646 standard; protein; 299 AA.
XX
AC AED14646;
XX
DT 01-DEC-2005 (first entry)
XX

DE Protein sequence of wild type A chain of shiga-like toxin 1.
XX
KW Toxin; therapeutic; protein engineering; drug screening; melanoma;
KW cytostatic; neoplasm; cancer.
XX
OS Escherichia coli O157:H7.
XX
FH Key Location/Qualifiers
FT Domain 1..238
FT /note = Toxic enzymatic domain
FT Region 242..261
FT /note= "Protease sensitive loop"
XX
PN WO2005092917-A1.
XX
PD 06-OCT-2005.
XX
PF 26-MAR-2004; 2004WO-CA000443.
XX
PR 26-MAR-2004; 2004WO-CA000443.
XX
PA (GARI/) GARIEPY J.
PA (WEIX/) WEI X.
XX
PI Gariepy J, Wei X;
XX
DR WPI; 2005-676984/69.
XX
PT New combinatorial protein library of protein species comprising an A
PT chain of a toxic protein into which an insert has been introduced, useful
PT or developing therapeutics targeted against specific cell types.
XX
PS Claim 4; SEQ ID NO 1; 34pp; English.
XX
CC The new invention relates to libraries of toxin mutants, and to methods
CC of using them in the development of therapeutics targets against specific
CC cell types. The libraries comprise proteins with an A chain of a
CC heteromeric toxic protein into which an insert has been introduced. The
CC insert is introduced into the protease-sensitive loop of the Shiga-like
CC toxin I A chain. The insert creates an artificial binding domain with the
CC A chain to create a toxic specificity which is independent and different
CC from normal specificity associated with the B chain binding domain.
CC Specifically, the insert is selected to bind to MUC-1 receptors. Also
CC given is a method of identifying and isolating a ligand that binds to a
CC specific target or receptor. This comprises screening the isolated
CC protein against cells expressing the target/receptor, to confirm their
CC toxicity for cells expressing the target or receptor. The toxin serves as
CC a reporter, and the death of the cells is indicative of receptor binding.
CC The invention provides a composition for treating melanoma and other
CC types of cancer. The present sequence is the wild type A chain of shiga-
CC like toxin 1.
XX
SQ Sequence 299 AA;

Query Match 100.0%; Score 114; DB 9; Length 299;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 248 CHHHASRVARMASDEFPSMC 267

RESULT 6
AAW06403
ID AAW06403 standard; protein; 315 AA.
XX
AC AAW06403;
XX
DT 25-FEB-1997 (first entry)
XX
DE Verotoxigenic E. coli toxin (VT1) subunit A.
XX
KW Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine;
KW haemolytic uraemic syndrome; detection.
XX

OS Escherichia coli.
XX
PN WO9630043-A1.
XX
PD 03-OCT-1996.
XX
PF 25-MAR-1996; 96WO-US004093.
XX
PR 24-MAR-1995; 95US-00410058.
XX
PA (OPHI-) OPHIDIAN PHARM INC.
XX
PI Carroll SB, Stafford DC, Padhye NV;
XX
DR WPI; 1996-505779/50.
DR N-PSDB; AAT42649.
XX
PT Compsn. contg. neutralising antitoxin against E.coli vero-toxin - used to
PT treat intoxicated individuals, and as a prophylactic against diarrhoeal
PT disease or extra-intestinal complications of E.coli infection.
XX
PS Example 6; Page 51; 101pp; English.
XX
CC Compositions containing neutralising antitoxin against one or more E.
CC coli verotoxin (VT) can be used to treat intoxicated adults and children
CC with enteric bacterial infections. They may also be used as prophylactics
CC e.g. as a vaccine, against diarrhoeal disease or the development of extra
CC -intestinal complications of E.coli infection, especially haemolytic
CC uraemic syndrome. The antitoxin can also be used to detect E. coli VT in
CC a sample. The VT is recombinant, preferably a fusion protein containing a
CC non-VT protein sequence and part of the E.coli VT1 or VT2 sequence
XX
SQ Sequence 315 AA;

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
|||
Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 7
AAW21702
ID AAW21702 standard; protein; 315 AA.
XX
AC AAW21702;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 26-SEP-1997 (first entry)
XX
DE Shiga-like toxin (SLT-1) RIP.
XX
KW pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat;
KW ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
XX
OS Bacteriophage H-19B.
XX
FH Key Location/Qualifiers
FT Region 145..155
FT /note= "Position of possible insertion of internal
FT peptide linker sequence"
XX
PN US5635384-A.
XX
PD 03-JUN-1997.
XX
PF 26-JAN-1995; 95US-00378761.
XX
PR 11-JUN-1990; 90US-00535636.
PR 09-DEC-1992; 92US-00987927.
XX

PA (DOWC) DOWELANCO.
XX
PI Hey TD, Morgan AER, Walsh TA;
XX
DR WPI; 1997-309831/28.
XX
PT Inactive precursor of maize ribosome-inactivating protein - also chimeric
PT ribosome-inactivating protein precursors containing internal linker
PT sequences.
XX
PS Claim 2; Col 113-116; 121pp; English.
XX
CC The sequences given in AAW21698-710 represent Ribosome Inactivating
CC Proteins (RIP's), which may be used in the construction of the proRIP of
CC the invention. The proRIP has a selectively removable, internal peptide
CC linker. The precursor sequence is incapable of inactivating eukaryotic
CC ribosomes, but can be converted by removal of the linker into a protein
CC having alpha and beta fragments and being capable of inactivating
CC eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein
CC synthesis. They possess a highly specific N-glycosidase activity which
CC cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 28S
CC RNA. RIP's selectively inhibit cellular proliferation of cells, e.g.
CC cancer cells and HIV-infected T cells. The inactive proRIP proteins make
CC it possible to provide protein synthesis inhibitors with uses in
CC practical and improved ways not before possible. The RIP can be used to
CC make cytotoxic conjugates. (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 315 AA;

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
||||||| |||||||||||||
Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 8
AAW25139
ID AAW25139 standard; protein; 315 AA.
XX
AC AAW25139;
XX
DT 25-MAR-2003 (revised)
DT 02-DEC-1997 (first entry)
XX
DE SLT-1 (a ribosome inhibitory protein) inactive precursor.
XX
KW Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
KW internal linker; Barley Translation Inhibitor; Trichosanthin;
KW Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP;
KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
KW post-translational modification; cancer; neoplasia; HIV; AIDS;
KW human immunodeficiency virus; acquired immune deficiency syndrome.
XX
OS Synthetic.
XX
PN US5646026-A.
XX
PD 08-JUL-1997.
XX
PF 07-JUN-1995; 95US-00485286.
XX
PR 11-JUN-1990; 90US-00535636.
PR 09-DEC-1992; 92US-00987927.
PR 26-JAN-1995; 95US-00378761.
XX
PA (DOWC) DOWELANCO.
XX
PI Hey TD, Morgan AER, Walsh TA;
XX
DR WPI; 1997-362934/33.
XX

PT DNA encoding pro-ribosome inactivating proteins - inactive precursors of
PT ribosome inactivating proteins; can be expressed in eukaryotic cells
PT without causing cell death.
XX
PS Claim 4; Col 115-116; 186pp; English.
XX
CC AAW25139 represents an SLT-1 (a ribosome inhibitory protein, RIP) protein
CC which was engineered to contain a selectively removable internal peptide
CC linker sequence separating the alpha and beta units of the RIP. When
CC separated the two units regain activity and are capable of inactivating
CC eukaryotic ribosomes and hence preventing protein production. Many
CC different RIPS may be produced with an internal linker including maize
CC RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and Saporin. The RIPS
CC can be used in the construction of therapeutic toxins targeted to
CC specific cells such as tumour cells via the attachment of a targeting
CC polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy
CC (see US4869903). There is interest in expressing RIP recombinantly in
CC host eukaryotic cells, because of the capacity to provide correct post-
CC translational processing. However, RIPS effectively inhibit protein
CC synthesis in eukaryotic cells resulting in cell death. Since the inactive
CC RIP proteins are not cytotoxic to eukaryotic cells, they can be
CC recombinantly expressed in such cells and then converted to active RIP
CC proteins. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 315 AA;

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 9
AAY96681
ID AAY96681 standard; protein; 315 AA.
XX
AC AAY96681;
XX
DT 26-SEP-2000 (first entry)
XX
DE E. coli verotoxin 1 subunit A.
XX
KW VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; food;
KW recombinant production; screening; dairy; anti-bacterial; vaccine.
XX
OS Escherichia coli.
XX
PN US6080400-A.
XX
PD 27-JUN-2000.
XX
PF 13-MAR-1997; 97US-00816977.
XX
PR 24-MAR-1995; 95US-00410058.
XX
PA (OPHI-) OPHIDIAN PHARM INC.
XX
PI Williams JA, Byrne LM;
XX
DR WPI; 2000-451195/39.
DR N-PSDB; AAA51194.
XX
PT Bacterial cell for recombinantly expressing bacterial toxins in large
PT quantities useful for immunization and treatment of bacterial infections,
PT comprises expression vector encoding bacterial toxin.
XX
PS Example 6; Col 69-71; 83pp; English.
XX
CC The invention relates to antitoxin therapy for humans and other animals.
CC Antitoxins which neutralize the pathologic effects of Escherichia coli
CC toxins are generated by immunization of avian hosts with recombinant
CC toxin fragments. The recombinant E. coli verotoxin (VT) is a fusion
CC protein comprising a non-verotoxin protein (especially an affinity tag)

CC fused to a portion of the VT-1 or VT-2 sequence. The VT B chains are
CC small proteins (approximately 8 kDa), so use of a small affinity tag was
CC preferred (i.e. polyhistidine). A polyhistidine affinity tag facilitates
CC single step affinity purification of subunits from periplasmic extracts.
CC However, due to poor recovery of his-tagged VT-1 A and VT-2 A chains,
CC expression of maltose binding protein (MBP) fused subunits was
CC undertaken. Due to the toxicity of the VT-2 B subunit, strict uninduced
CC promoter control is necessary to permit cell viability. Bacterial host
CC cells expressing a recombinant expression vector encoding a polyhistidine
CC affinity tag and a portion of the VT-2 B chain are claimed. The vector is
CC chosen from pET24hisVT2BL+, pET24hisVT2BL- and pET24VT2B, where "L+"
CC indicates that the vector encodes the preprotein form of the protein and
CC "L-" indicates that the vector encodes the mature form of the protein.
CC The bacterial cell is capable of expressing large quantities (40 mg/l) of
CC VT-2B. The toxins are useful for immunizing non-mammals and for detecting
CC bacterial toxins in environmental samples including soil, water,
CC industrial samples, biological samples and samples obtained from food and
CC dairy processing instruments

XX

SQ Sequence 315 AA;

Query Match 100.0%; Score 114; DB 3; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
 |||||||
Db 264 CHHHASRVARMASDEFFPSMC 283

RESULT 10

AAU77817

ID AAU77817 standard; protein; 315 AA.

XX

AC AAU77817;

XX

DT 05-JUN-2002 (first entry)

XX

DE E. coli verotoxin VT1-A chain protein.

XX

KW Verotoxin; VT1-A; antitoxin; antidiarrheal; antibacterial; haemostatic;
KW vaccine; haemorrhagic cystitis; balantitis; haemolytic uremic syndrome;
KW thrombotic thrombocytopenic purpura.

XX

OS Escherichia coli.

XX

PN US2002012658-A1.

XX

PD 31-JAN-2002.

XX

PF 16-JUN-1999; 99US-00334477.

XX

PR 13-MAR-1997; 97US-00816977.

XX

PA (WILL/) WILLIAMS J A.

PA (BYRN/) BYRNE L M.

PA (PUGH/) PUGH C S G.

XX

PI Williams JA, Byrne LM, Pugh CSG;

XX

DR WPI; 2002-205094/26.

DR N-PSDB; ABK11775.

XX

PT New recombinant expression vector encoding affinity tag and Escherichia
PT coli type 1 or type 2 verotoxin, useful for treating or preventing
PT diseases due to E. coli verotoxins and in producing vaccines.

XX

PS Example 6; Page 38-39; 98pp; English.

XX

CC This invention relates to a recombinant expression vector encoding an
CC affinity tag and protein comprising at least a portion of a bacterial
CC toxin consisting of Escherichia coli type 1 or type 2 verotoxin. The
CC expression vector can be used to produce recombinant verotoxin protein
CC which can be used to create a vaccine against diseases caused by E. coli
CC such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins
CC are useful for treating humans and animals intoxicated with a bacterial

CC toxin, particularly E. coli verotoxin. The antitoxins may also be used in
CC the preventative treatment and in diagnostic assays to detect the
CC presence of a toxin in a sample. The polypeptides derived from E. coli
CC verotoxins are useful as immunogens for the production of vaccines,
CC including multivalent vaccines and antitoxins, which can be administered
CC to a subject at risk of diarrhoeal disease or at risk of developing extra
CC -intestinal complications of E. coli infections, e.g. haemolytic uremic
CC syndrome, thrombotic thrombocytopenic purpura. The present sequence
CC represents the E.coli verotoxin protein VT1-A used to create the
CC expression vectors of the invention
XX

SQ Sequence 315 AA;

Query Match 100.0%; Score 114; DB 5; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
||| ||| ||| ||| ||| |||
Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 11

ADC00545

ID ADC00545 standard; protein; 315 AA.

XX

AC ADC00545;

XX

DT 04-DEC-2003 (first entry)

XX

DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 590.

XX

KW enterohaemorrhagic; anti-bacterial.

XX

OS Escherichia coli; O157:H7.

XX

PN JP2002355074-A.

XX

PD 10-DEC-2002.

XX

PF 24-JAN-2002; 2002JP-00015959.

XX

PR 24-JAN-2001; 2001JP-00112010.

XX

PA (UYTS-) UNIV TSUKUBA.

XX

DR WPI; 2003-451640/43.

XX

PT Enterohemorrhagic Escherichia coli O157:H7-specific nucleic acid molecule
PT and a polypeptide and its use, a polypeptide, a vector and a host cell.

XX

PS Claim 3; SEQ ID NO 590; 2067pp; Japanese.

XX

CC The invention relates to a novel enterohaemorrhagic Escherichia coli
CC O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
CC has anti-bacterial activity. The polypeptide can be used in detection
CC and/or treatment of O157:H7 infection. The nucleotide sequence of the
CC genome of Enterohaemorrhagic E. coli O157:H7 was determined. The present
CC sequence represents an E. coli O157:H7-specific polypeptide of the
CC invention.

XX

SQ Sequence 315 AA;

Query Match 100.0%; Score 114; DB 7; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
||| ||| ||| ||| |||
Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 12

ADH34319

ID ADH34319 standard; protein; 315 AA.

XX

AC ADH34319;
XX
DT 11-MAR-2004 (first entry)
XX
DE Verotoxin 1 (VT1) A subunit.
XX
KW Attenuated verotoxin; attenuated VT; mutant A subunit; troponin I;
KW fusion protein; cancer; cytostatic; verotoxin 1; VT1; A subunit.
XX
OS Escherichia coli; O157:H7.
XX
PN WO2003066854-A1.
XX
PD 14-AUG-2003.
XX
PF 03-FEB-2003; 2003WO-JP001043.
XX
PR 04-FEB-2002; 2002JP-00026577.
XX
PA (YOSH/) YOSHIDA H.
XX
PI Yoshida H, Liu X;
XX
DR WPI; 2003-646309/61.
XX
PT Attenuated verotoxin controls tumor growth for treatment of cancer.
XX
PS Disclosure; Fig 3; 56pp; Japanese.
XX
CC The invention relates to attenuated verotoxins (VTs) comprising mutations
CC in one or more of the regions spanning residues 167-172 or 202-207 of the
CC mature verotoxin A subunit. The invention also relates to the mutant
CC verotoxin A subunit and the DNA encoding it; anticancer agents containing
CC the novel mutant A subunit; a fusion protein comprising the mutant
CC verotoxin A subunit and a ligand, especially troponin I, which binds to a
CC cancer cell; a fusion gene encoding the mutant A subunit/troponin I
CC fusion protein; and vectors encoding either the mutant verotoxin A
CC subunit, or the fusion gene of the invention. The attenuated verotoxins,
CC A subunits, fusion proteins, and polynucleotides encoding them are useful
CC in the treatment of cancer. The present sequence represents the A subunit
CC of verotoxin 1 (VT1).
XX
SQ Sequence 315 AA;

Query Match 100.0%; Score 114; DB 7; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
||| ||| ||| ||| ||| ||| |||
Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 13
AEF18888
ID AEF18888 standard; protein; 315 AA.
XX
AC AEF18888;
XX
DT 09-MAR-2006 (first entry)
XX
DE Shiga toxin, SEQ:28.
XX
KW Transgenic plant; plant fungal disease; disease-resistance;
KW pathogen resistance; trichothecene; ribosome inactivating protein;
KW Shiga toxin; transgenic.
XX
OS Bacteriophage SC370..
XX
PN US2006005271-A1.
XX
PD 05-JAN-2006.
XX
PF 13-DEC-2004; 2004US-00010795.
XX
PR 12-DEC-2003; 2003US-0529348P.

XX
PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Tumer NE, Di R;
XX
DR WPI; 2006-078100/08.
DR N-PSDB; AEF18887.
XX
PT New transgenic plant that exhibits increased resistance to toxins
PT targeting eukaryotic ribosomal L3 protein compared to a non-transgenic
PT control plant, useful for providing resistance against trichothecene
PT fungal toxins.
XX
PS Disclosure; SEQ ID NO 28; 93pp; English.
XX
CC The invention relates to a transgenic plant comprising an exogenous
CC nucleic acid encoding at least the first 21 to 99 N-terminal amino acids
CC of a full length eukaryotic ribosomal protein L3 and which exhibits
CC increased resistance to toxins (such as trichothecene fungal toxins) that
CC target the eukaryotic ribosomal protein L3. The exogenous nucleic acid
CC may further encode a ribosome inactivating protein (RIP) that targets a
CC eukaryotic L3 ribosomal protein e.g., Pokeweed Antiviral Protein (PAP),
CC its variants PAP-v and PAP-II, or ricin or Shiga toxin. The invention
CC also relates to seed derived from the transgenic plant, and to a method
CC of producing transgenic plants of the invention which have increased
CC resistance to infestation by fungi that produce toxins that target the
CC eukaryotic L3 protein. The transgenic plants of the invention are
CC resistant to trichothecene mycotoxins such as those produced by Fusarium
CC species. The N-terminal L3 protein fragment confers better resistance to
CC trichothecenes than the full-length protein, although it does not contain
CC the trichodermin resistance mutation tcm-1 (W255C) of yeast L3 which is
CC known to confer resistance to trichothecenes. Also, when co-expressed
CC with a RIP, the N-terminal L3 protein fragment reduces or eliminates the
CC toxicity associated with RIP expression, meaning that RIPs such as wild-
CC type PAP can be expressed at much higher levels in plants of the
CC invention compared to plants which express the wild-type PAP alone. In
CC addition, PAP does not autoregulate (i.e., degrade its own mRNA) in the
CC presence of L3 N-terminal fragments, resulting in higher expression and
CC increased resistance to fungal diseases, and does not depurinate the RNA
CC of the cell, resulting in less toxicity. The present sequence represents
CC a Shiga toxin which can optionally be expressed by a transgenic plant of
CC the invention.
XX
SQ Sequence 315 AA;

Query Match 100.0%; Score 114; DB 10; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 14
AAW25786
ID AAW25786 standard; protein; 316 AA.
XX
AC AAW25786;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-MAR-1998 (first entry)
XX
DE Phage H19B shiga-like toxin.
XX
KW Shiga-like toxin; slt-A gene; hybrid protein; cell delivery;
KW cell binding ligand; translocation domain; diphtheria toxin B';
KW interleukin-2; T-cell lymphoma; organ rejection; therapy; ss.
XX
OS Bacteriophage H-19B.
XX
PN US5668255-A.
XX
PD 16-SEP-1997.
XX

PF 04-AUG-1993; 93US-00102387.
XX
PR 07-JUN-1984; 84US-00618199.
PR 25-APR-1985; 85US-00726808.
PR 07-JUN-1985; 85US-00742554.
PR 22-DEC-1989; 89US-00456095.
PR 14-JUN-1990; 90US-00538276.
PR 27-JUN-1991; 91US-00722484.
XX
PA (SERA-) SERAGEN INC.
XX
PI Murphy JR;
XX
DR WPI; 1997-470103/43.
DR N-PSDB; AAT91637.
XX
PT New hybrid molecules for delivery of agents to cells - comprise a binding
PT domain of a cell binding ligand and a portion of a trans-location domain
PT of a protein.
XX
PS Example 3; Fig 8A-C; 30pp; English.
XX
CC This protein comprises the Escherichia coli phage H19B Shiga-like toxin.
CC DNA (see AAT91637) encoding the A subunit of the Shiga-like toxin was
CC used to construct a Shiga-like toxin A-diphtheria toxin B'-interleukin-2
CC (SLTA-DTB'-IL2) gene that was expressed in E. coli. The hybrid protein
CC can be isolated and used to treat conditions involving over-production of
CC cells bearing IL2 receptors, such as certain T-cell lymphomas and organ
CC transplant rejection crises. The hybrid inactivates ribosomes in cells
CC bearing IL2 receptors, resulting in cessation of protein synthesis and
CC death of target cells. Claimed hybrid proteins comprise a translocation
CC domain and a cell binding domain from e.g. a hormone, growth factor or
CC protein toxin. The hybrid molecules can be used for the delivery of
CC agents (e.g. therapeutic genes, toxins, detectable labels) into cells.
CC The use of a translocation mechanism ensures that the hybrid will be
CC effective in relatively low doses, since a high proportion of the
CC substance of interest will be taken into the targeted cells. The hybrid
CC molecules can be manufactured as a single hybrid recombinant protein,
CC permitting reproducibility, consistency, and the precise control of
CC composition. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17
CC -OCT-2003 to standardise OS field)
XX
SQ Sequence 316 AA;

Query Match 100.0%; Score 114; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
|||
Db 264 CHHHASRVARMASDEFFPSMC 283

RESULT 15
AAW06407
ID AAW06407 standard; protein; 323 AA.
XX
AC AAW06407;
XX
DT 25-FEB-1997 (first entry)
XX
DE Histidine tagged verotoxigenic E. coli toxin (VT1) subunit A.
XX
KW Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine;
haemolytic uraemic syndrome; detection.
XX
OS Escherichia coli.
XX
PN WO9630043-A1.
XX
PD 03-OCT-1996.
XX
PF 25-MAR-1996; 96WO-US004093.
XX
PR 24-MAR-1995; 95US-00410058.
XX

PA (OPHI-) OPHIDIAN PHARM INC.
XX
PI Carroll SB, Stafford DC, Padhye NV;
XX
DR WPI; 1996-505779/50.
DR N-PSDB; AAT42663.
XX
PT Compsn. contg. neutralising antitoxin against E.coli vero-toxin - used to
PT treat intoxicated individuals, and as a prophylactic against diarrhoeal
PT disease or extra-intestinal complications of E.coli infection.
XX
PS Example 6; Page 61-62; 101pp; English.
XX
CC Compositions containing neutralising antitoxin against one or more E.
CC coli verotoxin (VT) can be used to treat intoxicated adults and children
CC with enteric bacterial infections. They may also be used as prophylactics
CC e.g. as a vaccine, against diarrhoeal disease or the development of extra
CC -intestinal complications of E.coli infection, especially haemolytic
CC uraemic syndrome. The antitoxin can also be used to detect E. coli VT in
CC a sample. The VT is recombinant, preferably a fusion protein containing a
CC non-VT protein sequence and part of the E.coli VT1 or VT2 sequence. This
CC is a histidine tagged version of subunit A of VT1 as expressed from the
CC vector pET-23b
XX
SQ Sequence 323 AA;

Query Match 100.0%; Score 114; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
|||||||||||||||||||
Db 264 CHHHASRVARMASDEFPSMC 283

Search completed: July 20, 2006, 09:43:44
Job time : 18.1993 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 56.rai.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:37:31 ; Search time 2.69373 Seconds
(without alignments)
649.885 Million cell updates/sec

Title: US-10-717-243-56
Perfect score: 114
Sequence: 1 CHHHASRVARMASDEFPSMC 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PECTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	114	100.0	20	1	US-07-988-430-58	Sequence 58, Appl
2	114	100.0	20	1	US-08-425-336-56	Sequence 56, Appl
3	114	100.0	20	1	US-08-488-113B-56	Sequence 56, Appl
4	114	100.0	20	1	US-08-477-484B-56	Sequence 56, Appl
5	114	100.0	20	1	US-08-646-360-56	Sequence 56, Appl
6	114	100.0	20	2	US-08-839-765-56	Sequence 56, Appl
7	114	100.0	20	2	US-09-136-389-56	Sequence 56, Appl
8	114	100.0	20	2	US-09-610-838-56	Sequence 56, Appl
9	114	100.0	20	2	US-09-711-485-56	Sequence 56, Appl
10	114	100.0	20	5	PCT-US92-09487-58	Sequence 58, Appl

11	114	100.0	315	1	US-08-378-761A-73	Sequence 73, Appl
12	114	100.0	315	1	US-08-485-286-73	Sequence 73, Appl
13	114	100.0	315	2	US-08-816-977-2	Sequence 2, Appli
14	114	100.0	315	2	US-09-334-477-2	Sequence 2, Appli
15	114	100.0	323	2	US-08-816-977-21	Sequence 21, Appl
16	114	100.0	323	2	US-09-334-477-21	Sequence 21, Appl
17	114	100.0	326	2	US-08-816-977-37	Sequence 37, Appl
18	114	100.0	326	2	US-09-334-477-37	Sequence 37, Appl
19	114	100.0	332	1	US-08-621-803-251	Sequence 251, App
20	114	100.0	332	2	US-09-217-352-251	Sequence 251, App
21	114	100.0	690	2	US-08-816-977-47	Sequence 47, Appl
22	114	100.0	690	2	US-09-334-477-47	Sequence 47, Appl
23	114	100.0	708	2	US-08-816-977-33	Sequence 33, Appl
24	114	100.0	708	2	US-09-334-477-33	Sequence 33, Appl
25	47	41.2	135	1	US-08-757-036-3	Sequence 3, Appli
26	46	40.4	204	2	US-09-252-991A-18665	Sequence 18665, A
27	45	39.5	413	2	US-09-328-352-5860	Sequence 5860, Ap
28	45	39.5	525	2	US-09-252-991A-28266	Sequence 28266, A
29	44	38.6	138	1	US-08-757-036-1	Sequence 1, Appli
30	44	38.6	297	1	US-08-180-761B-2	Sequence 2, Appli
31	44	38.6	318	2	US-08-816-977-6	Sequence 6, Appli
32	44	38.6	318	2	US-09-334-477-6	Sequence 6, Appli
33	44	38.6	319	1	US-08-180-761B-1	Sequence 1, Appli
34	44	38.6	326	2	US-08-816-977-25	Sequence 25, Appl
35	44	38.6	326	2	US-09-334-477-25	Sequence 25, Appl
36	44	38.6	329	2	US-08-816-977-39	Sequence 39, Appl
37	44	38.6	329	2	US-09-334-477-39	Sequence 39, Appl
38	44	38.6	360	2	US-09-252-991A-28104	Sequence 28104, A
39	44	38.6	433	2	US-09-344-882-26	Sequence 26, Appl
40	44	38.6	433	2	US-10-293-865-26	Sequence 26, Appl
41	44	38.6	450	2	US-09-252-991A-24440	Sequence 24440, A
42	44	38.6	575	2	US-09-107-532A-3910	Sequence 3910, Ap
43	44	38.6	694	2	US-08-816-977-49	Sequence 49, Appl
44	44	38.6	694	2	US-09-334-477-49	Sequence 49, Appl
45	44	38.6	711	2	US-08-816-977-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
 US-07-988-430-58
; Sequence 58, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-988-430-58

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 1 CHHHASRVARMASDEFPSMC 20

RESULT 2
US-08-425-336-56
; Sequence 56, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-425-336-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 1 CHHHASRVARMASDEFPSMC 20

RESULT 3
US-08-488-113B-56
; Sequence 56, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-113B-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 1 CHHHASRVARMASDEFPSMC 20

RESULT 4
US-08-477-484B-56
; Sequence 56, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-484B-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
 |||||||||||||||||||
Db 1 CHHHASRVARMASDEFPSMC 20

RESULT 5
US-08-646-360-56
; Sequence 56, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-646-360-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
Db 1 CHHHASRVARMASDEFFPSMC 20

RESULT 6
US-08-839-765-56
; Sequence 56, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA

; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-839-765-56

Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
Db 1 CHHHASRVARMASDEFFPSMC 20

RESULT 7
US-09-136-389-56
; Sequence 56, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-136-389-56

Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
||| ||| ||| ||| ||| ||| |||
Db 1 CHHHASRVARMASDEFPSMC 20

RESULT 8
US-09-610-838-56
; Sequence 56, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348

; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-610-838-56

Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
||| ||| ||| ||| ||| ||| |||
Db 1 CHHHASRVARMASDEFFPSMC 20

RESULT 9
US-09-711-485-56
; Sequence 56, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-711-485-56

Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 1 CHHHASRVARMASDEFPSMC 20

RESULT 10
PCT-US92-09487-58
; Sequence 58, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids

; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US92-09487-58

Query Match 100.0%; Score 114; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 1 CHHHASRVARMASDEFPSMC 20

RESULT 11
US-08-378-761A-73
; Sequence 73, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-73

Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 12
US-08-485-286-73
; Sequence 73, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-286-73

Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
Db 264 CHHHASRVARMASDEFFPSMC 283

RESULT 13
US-08-816-977-2
; Sequence 2, Application US/08816977
; Patent No. 6080400
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Byrne, Lisa M.
; APPLICANT: Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; TITLE OF INVENTION: Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,977
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230

; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-816-977-2

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSCMC 20
|||
Db 264 CHHHASRVARMASDEFPSCMC 283

RESULT 14
US-09-334-477-2
; Sequence 2, Application US/09334477
; Patent No. 6652857
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MackKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-334-477-2

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSCMC 20
|||
Db 264 CHHHASRVARMASDEFPSCMC 283

RESULT 15
US-08-816-977-21
; Sequence 21, Application US/08816977
; Patent No. 6080400
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Byrne, Lisa M.
; APPLICANT: Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; TITLE OF INVENTION: Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,977
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 323 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-816-977-21

Query Match 100.0%; Score 114; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 6.2e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 264 CHHHASRVARMASDEFPSMC 283

Search completed: July 20, 2006, 09:38:56
Job time : 3.69373 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 56.rapbm.

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This page gives you Search Results detail for the Application 10717243 and Search Result us-10-717-243-56.rapbm.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:40:12 ; Search time 6.49446 Seconds
(without alignments)
1426.491 Million cell updates/sec

Title: US-10-717-243-56
Perfect score: 114
Sequence: 1 CHHHASRVARMASDEFPSMC 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	114	100.0	20	4	US-10-127-890-56	Sequence 56, Appl
2	114	100.0	20	5	US-10-717-243-56	Sequence 56, Appl
3	114	100.0	293	3	US-09-792-793A-37	Sequence 37, Appl
4	114	100.0	293	4	US-10-375-209A-37	Sequence 37, Appl
5	114	100.0	315	3	US-09-334-477-2	Sequence 2, Appl
6	114	100.0	315	6	US-11-010-795-28	Sequence 28, Appl
7	114	100.0	323	3	US-09-334-477-21	Sequence 21, Appl
8	114	100.0	326	3	US-09-334-477-37	Sequence 37, Appl
9	114	100.0	332	3	US-09-765-527-251	Sequence 251, App
10	114	100.0	690	3	US-09-334-477-47	Sequence 47, Appl
11	114	100.0	708	3	US-09-334-477-33	Sequence 33, Appl

12	48	42.1	96	4	US-10-425-115-237717	Sequence 237717,
13	48	42.1	162	4	US-10-767-701-40168	Sequence 40168, A
14	47	41.2	74	4	US-10-424-599-224605	Sequence 224605,
15	47	41.2	135	3	US-09-962-021-3	Sequence 3, Appli
16	47	41.2	135	4	US-10-408-765A-20	Sequence 20, Appl
17	47	41.2	293	5	US-10-732-923-4254	Sequence 4254, Ap
18	47	41.2	294	4	US-10-437-963-194718	Sequence 194718,
19	46.5	40.8	345	4	US-10-424-599-200140	Sequence 200140,
20	46	40.4	19	5	US-10-502-882-10	Sequence 10, Appl
21	46	40.4	196	4	US-10-282-122A-66424	Sequence 66424, A
22	46	40.4	378	6	US-11-087-099-11797	Sequence 11797, A
23	45	39.5	380	4	US-10-437-963-116579	Sequence 116579,
24	44.5	39.0	250	4	US-10-369-493-10325	Sequence 10325, A
25	44.5	39.0	251	6	US-11-188-298-9123	Sequence 9123, Ap
26	44.5	39.0	275	4	US-10-425-115-220907	Sequence 220907,
27	44.5	39.0	280	4	US-10-425-114-52863	Sequence 52863, A
28	44.5	39.0	544	3	US-09-925-299-1004	Sequence 1004, Ap
29	44.5	39.0	544	3	US-09-925-299-1004	Sequence 1004, Ap
30	44	38.6	82	4	US-10-424-599-216625	Sequence 216625,
31	44	38.6	137	4	US-10-408-765A-1100	Sequence 1100, Ap
32	44	38.6	138	3	US-09-962-021-1	Sequence 1, Appli
33	44	38.6	249	4	US-10-156-761-13851	Sequence 13851, A
34	44	38.6	286	5	US-10-732-923-14451	Sequence 14451, A
35	44	38.6	293	4	US-10-424-599-223435	Sequence 223435,
36	44	38.6	318	3	US-09-334-477-6	Sequence 6, Appli
37	44	38.6	319	3	US-09-792-793A-38	Sequence 38, Appl
38	44	38.6	319	3	US-09-870-759-28	Sequence 28, Appl
39	44	38.6	319	3	US-09-751-708A-28	Sequence 28, Appl
40	44	38.6	319	4	US-10-375-209A-38	Sequence 38, Appl
41	44	38.6	319	4	US-10-428-817A-24	Sequence 24, Appl
42	44	38.6	319	5	US-10-937-758A-28	Sequence 28, Appl
43	44	38.6	319	5	US-10-503-415-2	Sequence 2, Appli
44	44	38.6	319	6	US-11-010-795-26	Sequence 26, Appl
45	44	38.6	326	3	US-09-334-477-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
 US-10-127-890-56
 ; Sequence 56, Application US/10127890
 ; Publication No. US20030166196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; Carroll, Stephen F.
 ; Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
 ; NUMBER OF SEQUENCES: 173
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/127,890
 ; FILING DATE: 23-Apr-2002
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/646,360
 ; FILING DATE: 13-MAY-1996
 ; APPLICATION NUMBER: PCT/US94/05348
 ; FILING DATE: 12-MAY-1994
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-127-890-56

Query Match 100.0%; Score 114; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 1 CHHHASRVARMASDEFPSMC 20

RESULT 2
US-10-717-243-56
; Sequence 56, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155

; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-717-243-56

Query Match 100.0%; Score 114; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 1 CHHHASRVARMASDEFPSMC 20

RESULT 3

US-09-792-793A-37

; Sequence 37, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Shigella dysenteriae
US-09-792-793A-37

Query Match 100.0%; Score 114; DB 3; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 242 CHHHASRVARMASDEFPSMC 261

RESULT 4

US-10-375-209A-37

; Sequence 37, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Shigella dysenteriae
US-10-375-209A-37

Query Match 100.0%; Score 114; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
Db 242 CHHHASRVARMASDEFPSMC 261

RESULT 5
US-09-334-477-2
; Sequence 2, Application US/09334477
; Patent No. US20020012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-334-477-2

Query Match 100.0%; Score 114; DB 3; Length 315;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
 |||||||
Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 6
US-11-010-795-28
; Sequence 28, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: DI, RONG
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 28
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Bacteriophage SC370

US-11-010-795-28

Query Match 100.0%; Score 114; DB 6; Length 315;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
||| ||| ||| ||| |||
Db 264 CHHHASRVARMASDEFFPSMC 283

RESULT 7

US-09-334-477-21
; Sequence 21, Application US/09334477
; Patent No. US20020012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 323 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-334-477-21

Query Match 100.0%; Score 114; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
||| ||| ||| ||| |||
Db 264 CHHHASRVARMASDEFFPSMC 283

RESULT 8

US-09-334-477-37
; Sequence 37, Application US/09334477
; Patent No. US20020012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease

; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-334-477-37

Query Match 100.0%; Score 114; DB 3; Length 326;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSCMC 20
Db 275 CHHHASRVARMASDEFPSCMC 294

RESULT 9
US-09-765-527-251
; Sequence 251, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 251:
US-09-765-527-251

Query Match 100.0%; Score 114; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
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Db 277 CHHHASRVARMASDEFPSMC 296

RESULT 10
US-09-334-477-47
; Sequence 47, Application US/09334477
; Patent No. US20020012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 690 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-334-477-47

Query Match 100.0%; Score 114; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
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Db 639 CHHHASRVARMASDEFPSMC 658

RESULT 11
US-09-334-477-33
; Sequence 33, Application US/09334477
; Patent No. US20020012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; Byrne, Lisa M.
; Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-334-477-33

Query Match 100.0%; Score 114; DB 3; Length 708;
Best Local Similarity 100.0%; Pred. No. 4.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
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Db 657 CHHHASRVARMASDEFPSMC 676

RESULT 12
US-10-425-115-237717
; Sequence 237717, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 237717
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_148383C.1.pep
US-10-425-115-237717

Query Match 42.1%; Score 48; DB 4; Length 96;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMSAD 14
Db 82 CHHHLARLGSATD 95

RESULT 13

US-10-767-701-40168
; Sequence 40168, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 40168
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C46914_1.pep
US-10-767-701-40168

Query Match 42.1%; Score 48; DB 4; Length 162;
Best Local Similarity 44.4%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPS 18
Db 44 CYHHHDNYAATVSTDFPS 61

RESULT 14

US-10-424-599-224605
; Sequence 224605, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 224605
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_44849C.1.pep
US-10-424-599-224605

Query Match 41.2%; Score 47; DB 4; Length 74;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 HHHASRVARMASDEFPS 17
Db 58 HGHGSKVSTLASSNFP 73

RESULT 15

US-09-962-021-3
; Sequence 3, Application US/09962021
; Patent No. US20020106737A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: HUMAN SQM1 PROTEIN HOMOLOG
; FILE REFERENCE: PF-0170-2 CON
; CURRENT APPLICATION NUMBER: US/09/962,021
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020106737A1 g180233
US-09-962-021-3

Query Match 41.2%; Score 47; DB 3; Length 135;
Best Local Similarity 44.4%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPS 18
! || : : | |||
Db 58 CAHHLIRLLKCKRDSFPS 75

Search completed: July 20, 2006, 09:43:18
Job time : 7.49446 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 56.rapbn.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:40:39 ; Search time 1.18081 Seconds
(without alignments)
976.754 Million cell updates/sec

Title: US-10-717-243-56
Perfect score: 114
Sequence: 1 CHHHASRVARMASDEFPSMC 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 208217 seqs, 57668156 residues

Total number of hits satisfying chosen parameters: 208217

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	44	38.6	419	7	US-11-056-355B-78105	Sequence 78105, A
2	44	38.6	430	7	US-11-056-355B-78104	Sequence 78104, A
3	44	38.6	433	7	US-11-056-355B-78103	Sequence 78103, A
4	43	37.7	175	7	US-11-056-355B-17381	Sequence 17381, A
5	43	37.7	313	6	US-10-449-902-45435	Sequence 45435, A
6	43	37.7	691	6	US-10-511-937-2568	Sequence 2568, Ap
7	43	37.7	691	7	US-11-293-697-4345	Sequence 4345, Ap
8	42	36.8	141	7	US-11-056-355B-107028	Sequence 107028,
9	42	36.8	141	7	US-11-056-355B-118267	Sequence 118267,

10	42	36.8	142	6	US-10-953-349-2640	Sequence 2640, Ap
11	42	36.8	142	7	US-11-056-355B-39187	Sequence 39187, A
12	42	36.8	142	7	US-11-056-355B-48973	Sequence 48973, A
13	42	36.8	142	7	US-11-056-355B-101571	Sequence 101571,
14	42	36.8	142	7	US-11-056-355B-112810	Sequence 112810,
15	42	36.8	244	7	US-11-056-355B-107027	Sequence 107027,
16	42	36.8	244	7	US-11-056-355B-118266	Sequence 118266,
17	42	36.8	245	6	US-10-953-349-2639	Sequence 2639, Ap
18	42	36.8	245	7	US-11-056-355B-39186	Sequence 39186, A
19	42	36.8	245	7	US-11-056-355B-48972	Sequence 48972, A
20	42	36.8	245	7	US-11-056-355B-101570	Sequence 101570,
21	42	36.8	245	7	US-11-056-355B-112809	Sequence 112809,
22	42	36.8	252	7	US-11-056-355B-101569	Sequence 101569,
23	42	36.8	252	7	US-11-056-355B-112808	Sequence 112808,
24	42	36.8	273	7	US-11-056-355B-107026	Sequence 107026,
25	42	36.8	273	7	US-11-056-355B-118265	Sequence 118265,
26	42	36.8	777	7	US-11-293-697-3189	Sequence 3189, Ap
27	41	36.0	230	6	US-10-449-902-49282	Sequence 49282, A
28	41	36.0	366	7	US-11-056-355B-80990	Sequence 80990, A
29	41	36.0	387	7	US-11-056-355B-80989	Sequence 80989, A
30	41	36.0	400	6	US-10-953-349-7204	Sequence 7204, Ap
31	41	36.0	408	6	US-10-953-349-7203	Sequence 7203, Ap
32	41	36.0	412	6	US-10-953-349-7202	Sequence 7202, Ap
33	41	36.0	437	6	US-10-504-120-32	Sequence 32, Appl
34	41	36.0	444	7	US-11-056-355B-80988	Sequence 80988, A
35	40	35.1	270	6	US-10-505-928-805	Sequence 805, App
36	40	35.1	270	6	US-10-449-902-40832	Sequence 40832, A
37	40	35.1	310	7	US-11-056-355B-18267	Sequence 18267, A
38	40	35.1	354	7	US-11-056-355B-18266	Sequence 18266, A
39	40	35.1	377	7	US-11-056-355B-18265	Sequence 18265, A
40	40	35.1	411	7	US-11-056-355B-50091	Sequence 50091, A
41	40	35.1	418	7	US-11-056-355B-77816	Sequence 77816, A
42	40	35.1	463	6	US-10-449-902-37660	Sequence 37660, A
43	40	35.1	477	7	US-11-056-355B-50090	Sequence 50090, A
44	40	35.1	484	7	US-11-056-355B-77815	Sequence 77815, A
45	40	35.1	493	6	US-10-953-349-2205	Sequence 2205, Ap

ALIGNMENTS

RESULT 1
 US-11-056-355B-78105
 ; Sequence 78105, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nickolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; TITLE OF INVENTION: Polypeptides Encoded Thereby
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIOR APPLICATION NUMBER: 60/544,190
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 78105
 ; LENGTH: 419
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: peptide
 ; LOCATION: (1)..(419)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12605737
 US-11-056-355B-78105

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Query Match          38.6%;  Score 44;  DB 7;  Length 419;
Best Local Similarity 41.2%;  Pred. No. 27;
Matches    7;  Conservative  5;  Mismatches   5;  Indels     0;  Gaps      0;

Qy      3 HHASRVARMASDEFPSM 19
       || |::|: ||  |:
Db      251 HHVQRLSRLLSDPRPTI 267
```

RESULT 2

US-11-056-355B-78104
; Sequence 78104, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 78104
; LENGTH: 430
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(430)
; OTHER INFORMATION: Ceres Seq. ID no. 12605736

US-11-056-355B-78104

Query Match 38.6%; Score 44; DB 7; Length 430;
Best Local Similarity 41.2%; Pred. No. 28;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 HHASRVARMASDEFPSM 19
|| |::|: || |:
Db 262 HHVQRLSRLLSDPRPTI 278

RESULT 3

US-11-056-355B-78103
; Sequence 78103, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 78103
; LENGTH: 433
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(433)
; OTHER INFORMATION: Ceres Seq. ID no. 12605735

US-11-056-355B-78103

Query Match 38.6%; Score 44; DB 7; Length 433;
Best Local Similarity 41.2%; Pred. No. 28;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 HHASRVARMASDEFPSM 19
|| |::|: || |:
Db 265 HHVQRLSRLLSDPRPTI 281

RESULT 4

US-11-056-355B-17381
; Sequence 17381, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby

; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 17381
; LENGTH: 175
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(175)
; OTHER INFORMATION: Ceres Seq. ID no. 12360562
US-11-056-355B-17381

Query Match 37.7%; Score 43; DB 7; Length 175;
Best Local Similarity 47.1%; Pred. No. 16;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 HHASRVARMASDEFPSM 19
:||| :|| | |||:
Db 106 NHASMMARSVTDSVPSV 122

RESULT 5

US-10-449-902-45435

; Sequence 45435, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45435
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45435

Query Match 37.7%; Score 43; DB 6; Length 313;
Best Local Similarity 35.0%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
| ||| || | : | :|
Db 14 CQHHQERQAATAGESAKKLC 33

RESULT 6

US-10-511-937-2568

; Sequence 2568, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937

; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2568
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2568

Query Match 37.7%; Score 43; DB 6; Length 691;
Best Local Similarity 33.3%; Pred. No. 65;
Matches 8; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

Qy 1 CHHHASRVARM---ASDEFPSMC 20
|| | : |:: : || | |
Db 87 CHTHEEKAKLLEINSDDESPECC 110

RESULT 7
US-11-293-697-4345
; Sequence 4345, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4345
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4345

Query Match 37.7%; Score 43; DB 7; Length 691;
Best Local Similarity 33.3%; Pred. No. 65;
Matches 8; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

Qy 1 CHHHASRVARM---ASDEFPSMC 20
|| | : |:: : || | |
Db 87 CHTHEEKAKLLEINSDDESPECC 110

RESULT 8
US-11-056-355B-107028
; Sequence 107028, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 107028
; LENGTH: 141
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(141)
; OTHER INFORMATION: Ceres Seq. ID no. 13621190

US-11-056-355B-107028

Query Match 36.8%; Score 42; DB 7; Length 141;
Best Local Similarity 42.1%; Pred. No. 18;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 HHHASRVARMASDEFPSMC 20
||: | |: | ||: |
Db 117 HHNGSPVSLAPSPVIPSVC 135

RESULT 9

US-11-056-355B-118267
; Sequence 118267, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 118267
; LENGTH: 141
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(141)
; OTHER INFORMATION: Ceres Seq. ID no. 13621190
US-11-056-355B-118267

Query Match 36.8%; Score 42; DB 7; Length 141;
Best Local Similarity 42.1%; Pred. No. 18;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 HHHASRVARMASDEFPSMC 20
||: | |: | ||: |
Db 117 HHNGSPVSLAPSPVIPSVC 135

RESULT 10

US-10-953-349-2640
; Sequence 2640, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2640
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2640

Query Match 36.8%; Score 42; DB 6; Length 142;
Best Local Similarity 42.1%; Pred. No. 18;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 HHHASRVARMASDEFPSMC 20
||: | |: | ||: |
Db 118 HHNGSPVSLAPSPVIPSVC 136

RESULT 11

US-11-056-355B-39187
; Sequence 39187, Application US/11056355B

; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 39187
; LENGTH: 142
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(142)
; OTHER INFORMATION: Ceres Seq. ID no. 13489531
US-11-056-355B-39187

Query Match 36.8%; Score 42; DB 7; Length 142;
Best Local Similarity 42.1%; Pred. No. 18;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 HHHASRVARMASDEFPSMC 20
||: ||: | ||:
Db 118 HHNGSPVSLAPSPVIPSVC 136

RESULT 12
US-11-056-355B-48973
; Sequence 48973, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 48973
; LENGTH: 142
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(142)
; OTHER INFORMATION: Ceres Seq. ID no. 13489531
US-11-056-355B-48973

Query Match 36.8%; Score 42; DB 7; Length 142;
Best Local Similarity 42.1%; Pred. No. 18;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 HHHASRVARMASDEFPSMC 20
||: ||: | ||:
Db 118 HHNGSPVSLAPSPVIPSVC 136

RESULT 13
US-11-056-355B-101571
; Sequence 101571, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B

; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 101571
; LENGTH: 142
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(142)
; OTHER INFORMATION: Ceres Seq. ID no. 13608191
US-11-056-355B-101571

Query Match 36.8%; Score 42; DB 7; Length 142;
Best Local Similarity 42.1%; Pred. No. 18;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 HHHASRVARMASDEFPSMC 20
||: | |: | ||: |
Db 118 HHNGSPVSLAPSPVIPSV 136

RESULT 14
US-11-056-355B-112810
; Sequence 112810, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 112810
; LENGTH: 142
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(142)
; OTHER INFORMATION: Ceres Seq. ID no. 13608191
US-11-056-355B-112810

Query Match 36.8%; Score 42; DB 7; Length 142;
Best Local Similarity 42.1%; Pred. No. 18;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 HHHASRVARMASDEFPSMC 20
||: | |: | ||: |
Db 118 HHNGSPVSLAPSPVIPSV 136

RESULT 15
US-11-056-355B-107027
; Sequence 107027, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 107027
; LENGTH: 244
; TYPE: prt
; ORGANISM: Arabidopsis thaliana

; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(244)
; OTHER INFORMATION: Ceres Seq. ID no. 13621189
US-11-056-355B-107027

Query Match 36.8%; Score 42; DB 7; Length 244;
Best Local Similarity 42.1%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 HHHASRVARMASDEFPSMC 20
||: | |: | ||: |
Db 220 HHNGSPVSLAPSPVIPSV 238

Search completed: July 20, 2006, 09:41:18
Job time : 1.18081 secs

SCORE 1.3 BuildDate: 12/06/2005

This page gives you **Search Results** detail for the Application 10717243 and Search Result us-10-71 start

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:36:32 ; Search time 1.51292 Seconds
(without alignments)
1271.939 Million cell updates/sec

Title: US-10-717-243-56
Perfect score: 114
Sequence: 1 CHHASRVARMASDEFFPSMC 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	114	100.0	315	1	A28626	Shigella toxin cha
2	114	100.0	315	1	XUBPH9	Shiga-like toxin c
3	114	100.0	315	2	JN0725	Shiga-like toxin I
4	114	100.0	315	2	F91000	Shiga toxin I subu
5	114	100.0	315	2	H85845	Shiga toxin I subu
6	114	100.0	315	2	A53887	Shiga-like toxin I
7	50.5	44.3	365	2	T08577	hypothetical prote
8	50	43.9	451	2	T33763	hypothetical prote
9	49	43.0	2152	2	T45583	hypothetical prote
10	47	41.2	135	2	A34653	cell adhesion prot
11	47	41.2	252	2	D95853	conserved hypothet
12	46	40.4	196	2	D83279	probable transcrip
13	46	40.4	319	2	I60446	Shiga-like cytotox
14	46	40.4	507	2	JC7855	pyridoxine 4-oxida
15	45	39.5	254	2	S72759	hypothetical prote
16	45	39.5	278	2	G70871	hypothetical prote
17	45	39.5	466	2	PC4296	nicotinic acetylch
18	44	38.6	252	2	T35998	probable DNA-bindin
19	44	38.6	308	2	AH3425	D-ribose-binding p
20	44	38.6	318	2	S01032	Shiga-like toxin I

21	44	38.6	319	2	I76713	variant shiga-like
22	44	38.6	319	2	A32360	shiga-like toxin I
23	44	38.6	319	2	S58343	Shiga-like toxin I
24	44	38.6	319	2	S21940	hypothetical prote
25	44	38.6	319	2	E90779	Shiga toxin 2 subu
26	44	38.6	319	2	G85640	Shiga toxin 2 subu
27	44	38.6	319	2	I54695	shiga-like toxin I
28	44	38.6	319	2	A53890	verocytotoxin A ch
29	44	38.6	320	2	S42608	shiga-like toxin -
30	44	38.6	433	2	T04594	aldehyde dehydroge
31	44	38.6	475	2	S45116	natriuretic peptid
32	44	38.6	535	2	A54155	natriuretic peptid
33	43	37.7	536	2	S71332	natriuretic peptid
34	43	37.7	540	1	OYHUCR	natriuretic peptid
35	43	37.7	1149	2	T20891	hypothetical prote
36	43	37.7	2437	2	S53611	MIBP1 protein - ra
37	43	37.7	2500	1	WMHUE2	HIV-EP2 enhancer-b
38	42	36.8	161	2	S76282	hypothetical prote
39	42	36.8	285	2	B82842	spermidine synthas
40	42	36.8	381	2	S58663	isocitrate dehydro
41	42	36.8	387	2	T13147	isocitrate dehydro
42	42	36.8	398	2	AD2944	fosmidomycin resis
43	42	36.8	398	2	F98338	fosmidomycin resis
44	42	36.8	404	2	AB0376	probable membrane
45	42	36.8	406	1	JC5041	fosmidomycin resis

ALIGNMENTS

RESULT 1
A28626
Shigella toxin chain A precursor - Shigella dysenteriae
N;Alternate names: shiga toxin chain A
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Shigella dysenteriae
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C;Accession: A28626; S04021
R;Strockbine, N.A.; Jackson, M.P.; Sung, L.M.; Holmes, R.K.; O'Brien, A.D.
J. Bacteriol. 170, 1116-1122, 1988
A;Title: Cloning and sequencing of the genes for Shiga toxin from Shigella dysenteriae type 1.
A;Reference number: A91864; MUID:88139166; PMID:2830229
A;Contents: Type 1 3818T
A;Accession: A28626
A;Molecule type: DNA
A;Residues: 1-315
A;Cross-references: UNIPROT:Q8X696; UNIPARC:UPI0000000DA9; GB:M19437; NID:g152784; PIDN:AAA98347.1; PID:g15
R;Kozlov, Y.V.; Kabishev, A.A.; Fedchenko, V.I.; Baev, A.A.
Dokl. Biochem. 295, 216-220, 1987
A;Title: Cloning and primary structure of Shigella toxin genes.
A;Reference number: S04021
A;Accession: S04021
A;Molecule type: DNA
A;Residues: 1-315
A;Cross-references: UNIPARC:UPI0000000DA9; EMBL:X07903; NID:g46946
C;Genetics:
A;Gene: stxA
C;Complex: heterohexamer of one A chain and five B chains (see PIR:XVEBBD)
C;Function:
A;Description: hydrolyzes the N-glycosidic bond of a specific adenine in 28S rRNA
C;Superfamily: Shigella toxin chain A
C;Keywords: cytotoxin; glycosidase; hexamer; hydrolase; RNA binding
F;1-22/Domain: signal sequence #status predicted
F;23-315/Product: Shigella toxin chain A #status predicted

Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
 |||||||
Db 264 CHHHASRVARMASDEFFPSMC 283

RESULT 2
XUBPH9

Shiga-like toxin chain A precursor - phage H19B
 C;Species: phage H19B
 A;Note: host Escherichia coli
 C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
 C;Accession: A27052
 R;Calderwood, S.B.; Auclair, F.; Donohue-Rolfe, A.; Keusch, G.T.; Mekalanos, J.J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4364-4368, 1987
 A;Title: Nucleotide sequence of the Shiga-like toxin genes of Escherichia coli.
 A;Reference number: A27052; MUID:87260808; PMID:3299365
 A;Accession: A27052
 A;Molecule type: DNA
 A;Residues: 1-315
 A;Cross-references: UNIPROT:P08026; UNIPARC:UPI000000043F; GB:M16625; NID:g215043; PIDN:AAA98099.1; PID:g21
 C;Genetics:
 A;Gene: sltA
 C;Superfamily: Shigella toxin chain A
 C;Keywords: toxin
 F;1-22/Domain: signal sequence #status predicted
 F;23-315/Product: Shiga-like toxin chain A #status predicted

```

  Query Match      100.0%;  Score 114;  DB 1;  Length 315;
  Best Local Similarity  100.0%;  Pred. No. 8e-11;
  Matches 20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

  Qy      1 CHHHASRVARMASDEFPSMC 20
          ||||||| | | | | | | | |
  Db      264 CHHHASRVARMASDEFPSMC 283
  
```

RESULT 3
JN0725
 Shiga-like toxin I chain A precursor [validated] - Escherichia coli
 C;Species: Escherichia coli
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
 C;Accession: JN0725; I53932; I68041; I68043; C61473; A61473; S47254; S47256; S47258
 R;Paton, A.W.; Paton, J.C.; Goldwater, P.N.; Heuzenroeder, M.W.; Manning, P.A.
 Gene 129, 87-92, 1993
 A;Title: Sequence of a variant Shiga-like toxin type-I operon of Escherichia coli O111:H-.
 A;Reference number: JN0725; MUID:93328129; PMID:8335264
 A;Accession: JN0725
 A;Molecule type: DNA
 A;Residues: 1-315
 A;Cross-references: UNIPROT:Q47647; UNIPARC:UPI0000BC490; GB:L04539; NID:g147832; PIDN:AAA71893.1; PID:g14
 A;Experimental source: serotype O111:H(-)
 R;Paton, A.W.; Beutin, L.; Paton, J.C.
 Gene 153, 71-74, 1995
 A;Title: Heterogeneity of the amino-acid sequences of Escherichia coli Shiga-like toxin type-I operons.
 A;Reference number: I53932; MUID:95189106; PMID:7883188
 A;Accession: I53932
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-170,'S',172-248,'E',250-315
 A;Cross-references: UNIPARC:UPI00000BA3CB; EMBL:Z36899; NID:g534987; PIDN:CAA85366.1; PID:g534988
 A;Experimental source: serotype O48:H21
 A;Note: submitted to the EMBL Data Library, August 1994
 A;Accession: I68041
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-131,'S',133-170,'S',172-315
 A;Cross-references: UNIPARC:UPI00000B9ECB; EMBL:Z36900; NID:g535054; PIDN:CAA85368.1; PID:g535055
 A;Experimental source: serotype O111:H(-)
 A;Note: submitted to the EMBL Data Library, August 1994
 A;Accession: I68043
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-170,'S',172-250,'V',252-273,'IVPN',278-284,'V',286-308,'I',310-311,'A',313-315
 A;Cross-references: UNIPARC:UPI0000055D32; EMBL:Z36901; NID:g535088; PIDN:CAA85370.1; PID:g535089
 A;Experimental source: serotype OX3:H8
 R;Takao, T.; Tanabe, T.; Hong, Y.M.; Shimonishi, Y.; Kurazono, H.; Yutsudo, T.; Sasakawa, C.; Yoshikawa, M.
 Microb. Pathog. 5, 357-369, 1988
 A;Title: Identity of molecular structure of Shiga-like toxin I (VT1) from Escherichia coli O157:H7 with tha
 A;Reference number: A61473
 A;Accession: C61473
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-170,'S',172-315

A;Cross-references: UNIPARC:UPI0000000DA9
A;Experimental source: strain O157:H7
A;Accession: A61473
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-51;62-76;107-132,'XX',135-136;183-192;202-224,'XX',227-241;276-282,291-294,'X',296-299,'X',3
A;Cross-references: UNIPARC:UPI00001766F7; UNIPARC:UPI00001766F8; UNIPARC:UPI00001766F9; UNIPARC:UPI0000176
A;Experimental source: strain O157:H7
C;Genetics:
A;Gene: SLT-1A
C;Superfamily: Shigella toxin chain A
C;Keywords: disulfide bond; toxin
F;1-22/Domain: signal sequence #status predicted
F;23-315/Product: Shiga-like toxin I chain A #status experimental

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
Db 264 CHHHASRVARMASDEFFPSMC 283

RESULT 4
F91000
Shiga toxin I subunit A precursor [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F91000
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Ohtsubo, E.; Naka
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315
A;Cross-references: UNIPROT:Q8X696; UNIPARC:UPI0000000DA9; GB:BA000007; PIDN:BAB36397.1; PID:g13362443; GSP
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs2974
C;Superfamily: Shigella toxin chain A

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
Db 264 CHHHASRVARMASDEFFPSMC 283

RESULT 5
H85845
Shiga toxin I subunit A precursor [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85845
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85845
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315
A;Cross-references: UNIPROT:Q8X696; UNIPARC:UPI0000000DA9; GB:AE005174; NID:g12516395; PIDN:AAG57228.1; GSP
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: stx1A
C;Superfamily: Shigella toxin chain A

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
||| ||| ||| ||| ||| |||
Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 6
A53887
Shiga-like toxin I A chain precursor - phage 933J
C;Species: phage 933J
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: A53887
R;Jackson, M.P.; Newland, J.W.; Holmes, R.K.; O'Brien, A.D.
Microb. Pathog. 2, 147-153, 1987
A;Title: Nucleotide sequence analysis of the structural genes for Shiga-like toxin I encoded by bacteriophaga
A;Reference number: A53887; MUID:89180929; PMID:3333796
A;Accession: A53887
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315
A;Cross-references: UNIPROT:P08026; UNIPARC:UPI00000043F; GB:M19473; NID:g215072; PIDN:AAA98151.1; PID:g21
C;Superfamily: Shigella toxin chain A

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
||| ||| ||| ||| |||
Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 7
T08577
hypothetical protein T22F8.190 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08577
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuell
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16442
A;Accession: T08577
A;Molecule type: DNA
A;Residues: 1-365
A;Cross-references: UNIPROT:Q9T035; UNIPARC:UPI00000A6AFC; EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.190
A;Experimental source: cultivar Columbia; BAC clone T22F8
C;Genetics:
A;Gene: ATSP:T22F8.190
A;Map position: 4
C;Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 44.3%; Score 50.5; DB 2; Length 365;
Best Local Similarity 47.8%; Pred. No. 1.9;
Matches 11; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

Qy 1 CHHHASRVA---RMASDEFPSMC 20
| | | | |:| |:|:|| |
Db 140 CRSHTWREAPSMRVARDDFPSTC 162

RESULT 8
T33763
hypothetical protein Y55H10A.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33763
R;Antoniou, B.; Smith, A.; Gibson, A.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid Y55H10A.
A;Reference number: Z21402
A;Accession: T33763
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-451
A;Cross-references: UNIPROT:Q9TYW1; UNIPARC:UPI000007570D; EMBL:AF100675; PIDN: AAC69004.1; GSPDB:GN00022; C
A;Experimental source: strain Bristol N2; clone Y55H10A

C;Genetics:
A;Gene: CESP:Y55H10A.1
A;Map position: 4
A;Introns: 29/2; 57/1; 95/3; 233/1; 319/3
C;Superfamily: Caenorhabditis elegans hypothetical protein Y55H10A.1

Query Match 43.9%; Score 50; DB 2; Length 451;
Best Local Similarity 58.8%; Pred. No. 2.8;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 HHHASRVARMASDEFPS 18
| :||| |:!:||| |
Db 151 HEKSSRVKRVATDEFNS 167

RESULT 9
T45583
hypothetical protein F11C1.210 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45583
R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; Mayer, K.F.X.; Lemcke,
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23007
A;Accession: T45583
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2152
A;Cross-references: UNIPROT:Q9SND1; UNIPARC:UPI000009D156; EMBL:AL132976
A;Experimental source: cultivar Columbia; BAC clone F11C1
C;Genetics:
A;Map position: 3
A;Introns: 53/3; 411/2; 1479/3; 1543/2; 1592/3; 1659/1; 1750/1; 1965/3
A;Note: F11C1.210

Query Match 43.0%; Score 49; DB 2; Length 2152;
Best Local Similarity 41.2%; Pred. No. 20;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 HHASRVARMASDEFPSM 19
| | :|| : :|||:
Db 131 HHVEKVATLRGEDFPSL 147

RESULT 10
A34653
cell adhesion protein SQM1 - human
C;Species: Homo sapiens (man)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34653
R;Wong, Y.C.; Tsao, S.W.; Kakefuda, M.; Bernal, S.D.
Biochem. Biophys. Res. Commun. 166, 984-992, 1990
A;Title: cDNA cloning of a novel cell adhesion protein expressed in human squamous carcinoma cells.
A;Reference number: A34653; MUID:90147818; PMID:2302251
A;Accession: A34653
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135
A;Cross-references: UNIPROT:P17568; UNIPARC:UPI000014AAD6; GB:M33374; NID:g180232; PIDN:AAA35675.1; PID:g18
C;Keywords: cell adhesion

Query Match 41.2%; Score 47; DB 2; Length 135;
Best Local Similarity 44.4%; Pred. No. 2.5;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPS 18
| || |: : | |||:
Db 58 CAHHLIRLLKCKRDSFPS 75

RESULT 11
D95853
conserved hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: D95853

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernandez-Lucas, I.; Beck
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizob
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95853
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252
A;Cross-references: UNIPROT:Q92X70; UNIPARC:UPI00000CB3EA; GB:AL591985; PIDN:CAC48492.1; PID:g15139964; GSP
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Barnett, M.J.;
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, V.; Masuy, D.; Pal
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMb20092
A;Genome: plasmid

Query Match 41.2%; Score 47; DB 2; Length 252;
Best Local Similarity 52.9%; Pred. No. 4.7;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFP 17
| | | :|| ||| |
Db 224 CRVHGSTLARSASDHLP 240

RESULT 12
D83279
probable transcription regulator PA2931 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83279
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brinkman, F.S.L.; Huf
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83279
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-196
A;Cross-references: UNIPROT:Q9HZR6; UNIPARC:UPI00000C588E; GB:AE004719; GB:AE004091; NID:g9949021; PIDN:AAG
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2931

Query Match 40.4%; Score 46; DB 2; Length 196;
Best Local Similarity 69.2%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 VARMASDEFPSMC 20
||| ||||| |
Db 95 VARFCSDEFPRGC 107

RESULT 13
I60446
Shiga-like cytotoxin subunit A - Escherichia coli
N;Alternate names: shiga-like toxin II variant chain A
C;Species: Escherichia coli
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I60446; I57048; S31420
R;Paton, A.W.; Paton, J.C.; Heuzenroeder, M.W.; Goldwater, P.N.; Manning, P.A.
Microb. Pathog. 13, 225-236, 1992
A;Title: Cloning and nucleotide sequence of a variant Shiga-like toxin II gene from Escherichia coli OX3:H2
A;Reference number: I60446; MUID:93180660; PMID:1291844
A;Accession: I60446
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-319
A;Cross-references: UNIPROT:Q03037; UNIPARC:UPI00000BEE9B; EMBL:X65949; NID:g49089; PIDN:CAA46767.1; PID:g4
R;Paton, A.W.; Paton, J.C.; Manning, P.A.
Microb. Pathog. 15, 77-82, 1993
A;Title: Polymerase chain reaction amplification, cloning and sequencing of variant Escherichia coli Shiga-

A;Reference number: I57048; MUID:94018566; PMID:8412629
A;Accession: I57048
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-197, 'G', 199-319
A;Cross-references: UNIPARC:UPI000016F4EF; GB:L11078; NID:g304950; PIDN:AAA16360.1; PID:g304951
C;Superfamily: Shigella toxin chain A
C;Keywords: cytotoxin

Query Match 40.4%; Score 46; DB 2; Length 319;
Best Local Similarity 35.0%; Pred. No. 8.7;
Matches 7; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
||| :| | ::| |
Db 263 CHHQGARSVRAVNEEIQPEC 282

RESULT 14
JC7855
pyridoxine 4-oxidase (EC 1.1.3.12) - Microbacterium luteolum YK-1
N;Alternate names: PN 4-oxidase; pyridoxin 4-oxidase
C;Species: Microbacterium luteolum YK-1
C;Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change 05-Oct-2004
C;Accession: JC7855; PC7192
R;Kaneda, Y.; Ohnishi, K.; Yagi, T.
Biosci. Biotechnol. Biochem. 66, 1022-1031, 2002
A;Title: Purification, Molecular cloning, and characterization of pyridoxine 4-oxidase from Microbacterium
A;Reference number: JC7855; MUID:22087109; PMID:12092811
A;Accession: JC7855
A;Molecule type: DNA
A;Residues: 1-507
A;Cross-references: UNIPARC:UPI000017CE48; DDBJ:AB049341
A;Experimental source: strain YK-1
A;Accession: PC7192
A;Molecule type: protein
A;Residues: 2-20;348-364
A;Cross-references: UNIPARC:UPI000017CE49; UNIPARC:UPI000017CE4A
C;Comment: This enzyme that is an FAD-dependent enzyme and a monomeric protein belongs to the glucose-metha
C;Genetics:
A;Gene: pno
C;Superfamily: alcohol oxidase
C;Keywords: oxidoreductase

Query Match 40.4%; Score 46; DB 2; Length 507;
Best Local Similarity 57.1%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 HHHASRVARMASDE 15
|||| | ||| |||
Db 446 HHHPSGTCRMGKDE 459

RESULT 15
S72759
hypothetical protein B1496_C2_188 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72759; T11014
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B1496.
A;Reference number: S72695
A;Accession: S72759
A;Molecule type: DNA
A;Residues: 1-254
A;Cross-references: UNIPROT:Q49688; UNIPARC:UPI00000D433C; EMBL:U00013; NID:g466868; PIDN:AAA17126.1; PID:g
R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z16918
A;Accession: T11014
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-254
A;Cross-references: UNIPARC:UPI00000D433C; EMBL:Z99125; NID:g2398683; PIDN:CAB16173.1; PID:g2398708
C;Genetics:

A;Gene: MLCL536.29c

A;Start codon: GTG

Query Match 39.5%; Score 45; DB 2; Length 254;
Best Local Similarity 45.5%; Pred. No. 10;
Matches 10; Conservative 2; Mismatches 4; Indels 6; Gaps 2;

Qy 1 CHHH--ASRVARMASDEFPSMC 20
| ||| | || :||| :|
Db 196 CQHHCPVSHVA---EEFPELC 213

Search completed: July 20, 2006, 09:37:23
Job time : 2.51292 secs

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 56.rup.

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OM protein - protein search, using sw.model

Run on: July 20, 2006, 09:36:29 ; Search time 20.5535 Seconds
(without alignments)
900.105 Million cell updates/sec

Title: US-10-717-243-56
Perfect score: 114
Sequence: 1 CHHHASRVARMASDEFPSMC 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB	ID	Description
<hr/>						
1	114	100.0	222	2	Q5ZPW9_ECOLI	Q5zpw9 escherichia
2	114	100.0	236	2	Q5ZPX0_ECOLI	Q5zpx0 escherichia
3	114	100.0	237	2	Q5ZPX1_ECOLI	Q5zpx1 escherichia
4	114	100.0	240	2	Q5ZPX2_ECOLI	Q5zpx2 escherichia
5	114	100.0	242	2	Q5ZPX4_ECOLI	Q5zpx4 escherichia
6	114	100.0	243	2	Q5ZPX3_ECOLI	Q5zpx3 escherichia
7	114	100.0	243	2	Q5ZPX5_ECOLI	Q5zpx5 escherichia
8	114	100.0	248	2	Q5ZPX6_ECOLI	Q5zpx6 escherichia
9	114	100.0	254	2	Q5ZPX8_ECOLI	Q5zpx8 escherichia
10	114	100.0	259	2	Q5ZPX9_ECOLI	Q5zpx9 escherichia
11	114	100.0	276	2	Q5ZPY0_ECOLI	Q5zpy0 escherichia
12	114	100.0	313	2	Q7WZI8_ECO57	Q7wzi8 escherichia
13	114	100.0	315	1	SLTA_BPH19	P08026 bacterioph
14	114	100.0	315	1	SLTA_BPH30	P10149 bacterioph
15	114	100.0	315	2	Q5MBW7_9CAUD	Q5mbw7 stx1-conver

16	114	100.0	315	2	Q6LDT4_9VIRU	Q6ldt4 coliphage 9
17	114	100.0	315	2	Q776E8_9CAUD	Q776e8 stx1 conver
18	114	100.0	315	2	Q777W4_9VIRU	Q777w4 bacteriopha
19	114	100.0	315	2	Q779K4_9CAUD	Q779k4 shigella so
20	114	100.0	315	2	Q77YB9_BPH19	Q77yb9 bacteriopha
21	114	100.0	315	2	Q7AYI8_9VIRU	Q7ayi8 bacteriopha
22	114	100.0	315	2	Q32GM1_SHIDS	Q32gml shigella dy
23	114	100.0	315	2	Q47638_ECOLI	Q47638 escherichia
24	114	100.0	315	2	Q47639_ECOLI	Q47639 escherichia
25	114	100.0	315	2	Q47647_ECOLI	Q47647 escherichia
26	114	100.0	315	2	Q7B2T8_SHISO	Q7b2t8 shigella so
27	114	100.0	315	2	Q7BQ99_SHIDY	Q7bq99 shigella dy
28	114	100.0	315	2	Q7WZI7_ECO57	Q7wzi7 escherichia
29	114	100.0	315	2	Q8L170_ECOLI	Q8l170 escherichia
30	114	100.0	315	2	Q8X696_ECOLI	Q8x696 escherichia
31	114	100.0	315	2	Q9FBI2_SHIDY	Q9fbi2 shigella dy
32	114	100.0	315	2	Q7AK38_ECO57	Q7ak38 escherichia
33	114	100.0	315	2	Q6H9W4_9CAUD	Q6h9w4 phage bp-47
34	105	92.1	315	2	Q83XK3_ECOLI	Q83xk3 escherichia
35	96	84.2	315	2	Q94M00_9VIRU	Q94m00 bacteriopha
36	96	84.2	315	2	Q47640_ECOLI	Q47640 escherichia
37	96	84.2	315	2	Q8VV67_ECOLI	Q8vv67 escherichia
38	90	78.9	315	2	Q8VV64_ECOLI	Q8vv64 escherichia
39	89	78.1	251	2	Q5ZPX7_ECOLI	Q5zpx7 escherichia
40	86	75.4	315	2	Q8L168_ECOLI	Q8l168 escherichia
41	52	45.6	427	2	Q4UWU4_XANC8	Q4uwu4 xanthomonas
42	52	45.6	427	2	Q8P7A8_XANCP	Q8p7a8 xanthomonas
43	52	45.6	555	2	Q3XRP7_9PROT	Q3xrp7 magnetococc
44	51	44.7	274	2	Q2RSZ4_RHORU	Q2rsz4 rhodospiril
45	50.5	44.3	365	2	Q9T035_ARATH	Q9t035 arabidopsis

ALIGNMENTS

RESULT 1
Q5ZPW9_ECOLI
ID Q5ZPW9_ECOLI PRELIMINARY; PRT; 222 AA.
AC Q5ZPW9;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Verocytotoxin 1 (Fragment).
GN Name=VT1;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=372;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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DR EMBL; AJ537526; CAD68999.1; -; Genomic_DNA.
DR SMR; Q5ZPW9; 1-222.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PRO0396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1 1
FT NON_TER 222 222
SQ SEQUENCE 222 AA; 24698 MW; F29BF3CE24419E29 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 5.5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
|||||||||||||||||

RESULT 2

Q5ZPX0_ECOLI

ID Q5ZPX0_ECOLI PRELIMINARY; PRT; 236 AA.

AC Q5ZPX0;

DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.

DT 23-NOV-2004, sequence version 1.

DT 07-FEB-2006, entry version 8.

DE Verocytotoxin 1 (Fragment).

GN Name=VT1;

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=348;

RA Catarame T.M.;

RT "Rapid Diagnostic Methods for Food Borne Pathogens.";

RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

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CC -----

DR EMBL; AJ537525; CAD68998.1; -; Genomic_DNA.

DR SMR; Q5ZPX0; 1-236.

DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.

DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

DR InterPro; IPRO001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS00275; SHIGA_RICIN; 1.

FT NON_TER 1 1

FT NON_TER 236 236

SQ SEQUENCE 236 AA; 26045 MW; F8EEDF81890F04C0 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 236;

Best Local Similarity 100.0%; Pred. No. 5.9e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFFPSMC 20
 |||||||||||||||||||

Db 207 CHHHASRVARMASDEFFPSMC 226

RESULT 3

Q5ZPX1_ECOLI

ID Q5ZPX1_ECOLI PRELIMINARY; PRT; 237 AA.

AC Q5ZPX1;

DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.

DT 23-NOV-2004, sequence version 1.

DT 07-FEB-2006, entry version 8.

DE Verocytotoxin 1 (Fragment).

GN Name=VT1;

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=333;

RA Catarame T.M.;

RT "Rapid Diagnostic Methods for Food Borne Pathogens.";

RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

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DR EMBL; AJ537524; CAD68997.1; -; Genomic_DNA.

DR SMR; Q5ZPX1; 1-237.

DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.

DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

DR InterPro; IPRO001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PRO0396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1 1
FT NON_TER 237 237
SQ SEQUENCE 237 AA; 26183 MW; D578EEDF81890F04 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 5.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
|||||||||||||||||||
Db 207 CHHHASRVARMASDEFPSMC 226

RESULT 4
Q5ZPX2_ECOLI
ID Q5ZPX2_ECOLI PRELIMINARY; PRT; 240 AA.
AC Q5ZPX2;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Verocytotoxin 1 (Fragment).
GN Name=VT1;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=359;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

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DR EMBL; AJ537523; CAD68996.1; -; Genomic_DNA.
DR SMR; Q5ZPX2; 1-240.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PRO0396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1 1
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 26538 MW; B46AA23578EEDF81 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
|||||||||||||||||||
Db 207 CHHHASRVARMASDEFPSMC 226

RESULT 5
Q5ZPX4_ECOLI
ID Q5ZPX4_ECOLI PRELIMINARY; PRT; 242 AA.
AC Q5ZPX4;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Verocytotoxin 1 (Fragment).
GN Name=VT1;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=354;
RA Catarame T.M.;

RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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 DR EMBL; AJ537521; CAD68994.1; -; Genomic_DNA.
 DR SMR; Q5ZPX4; 1-242.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPRO001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 FT NON_TER 1 1
 FT NON_TER 242 242
 SQ SEQUENCE 242 AA; 26615 MW; A32A72928BB03D43 CRC64;

 Query Match 100.0%; Score 114; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 6.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 CHHHASRVARMASDEFPSMC 20
 |||||||
 Db 216 CHHHASRVARMASDEFPSMC 235

RESULT 6
 Q5ZPX3_ECOLI
 ID Q5ZPX3_ECOLI PRELIMINARY; PRT; 243 AA.
 AC Q5ZPX3;
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
 DT 23-NOV-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Verocytotoxin 1 (Fragment).
 GN Name=VT1;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=352;
 RA Catarame T.M.;
 RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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 DR EMBL; AJ537522; CAD68995.1; -; Genomic_DNA.
 DR SMR; Q5ZPX3; 1-243.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPRO001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 FT NON_TER 1 1
 FT NON_TER 243 243
 SQ SEQUENCE 243 AA; 26765 MW; 1E58F46958FD9469 CRC64;

 Query Match 100.0%; Score 114; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 6.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 CHHHASRVARMASDEFPSMC 20
 |||||||
 Db 209 CHHHASRVARMASDEFPSMC 228

RESULT 7
 Q5ZPX5_ECOLI
 ID Q5ZPX5_ECOLI .PRELIMINARY; PRT; 243 AA.
 AC Q5ZPX5;
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.

DT 23-NOV-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Verocytotoxin 1 (Fragment).
 GN Name=VT1;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=381;
 RA Catarame T.M.;
 RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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 CC
 DR EMBL; AJ537520; CAD68993.1; -; Genomic_DNA.
 DR SMR; Q5ZPX5; 1-243.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 FT NON_TER 1 1
 FT NON_TER 243 243
 SQ SEQUENCE 243 AA; 26617 MW; 4A69E4A3538DE250 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 6.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
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 Db 218 CHHHASRVARMASDEFPSMC 237

RESULT 8
 Q5ZPX6_ECOLI
 ID Q5ZPX6_ECOLI PRELIMINARY; PRT; 248 AA.
 AC Q5ZPX6;
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
 DT 23-NOV-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Verocytotoxin 1 (Fragment).
 GN Name=VT1;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CH1;
 RA Catarame T.M.;
 RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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 DR EMBL; AJ537519; CAD68992.1; -; Genomic_DNA.
 DR SMR; Q5ZPX6; 4-248.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 FT NON_TER 1 1
 FT NON_TER 248 248
 SQ SEQUENCE 248 AA; 27190 MW; 653792826D462FED CRC64;

Query Match 100.0%; Score 114; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHHHASRVARMASDEFPSMC 20
Db 222 CHHHASRVARMASDEFPSMC 241

RESULT 9
Q5ZPX8_ECOLI
ID Q5ZPX8_ECOLI PRELIMINARY; PRT; 254 AA.
AC Q5ZPX8;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Verocytotoxin 1 (Fragment).
GN Name=VT1;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=361;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; AJ537517; CAD68990.1; -; Genomic_DNA.
DR SMR; Q5ZPX8; 1-254.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPRO01574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1 1
FT NON_TER 254 254
SQ SEQUENCE 254 AA; 27842 MW; AC3EF7F69D9D1A52 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 6.4e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHHHASRVARMASDEFPSMC 20
Db 228 CHHHASRVARMASDEFPSMC 247

RESULT 10
Q5ZPX9_ECOLI
ID Q5ZPX9_ECOLI PRELIMINARY; PRT; 259 AA.
AC Q5ZPX9;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Verocytotoxin 1 (Fragment).
GN Name=VT1;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=332;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; AJ537516; CAD68989.1; -; Genomic_DNA.
DR SMR; Q5ZPX9; 15-259.

DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 FT NON_TER 1 1
 FT NON_TER 259 259
 SQ SEQUENCE 259 AA; 28482 MW; 774B2B9CD18F9175 CRC64;

 Query Match 100.0%; Score 114; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 6.5e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 CHHHASRVARMASDEFPSMC 20
 |||||||
 Db 233 CHHHASRVARMASDEFPSMC 252

RESULT 11
 Q5ZPY0_ECOLI
 ID Q5ZPY0_ECOLI PRELIMINARY; PRT; 276 AA.
 AC Q5ZPY0;
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
 DT 23-NOV-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Verocytotoxin 1 (Fragment).
 GN Name=VT1;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=378;
 RA Catarame T.M.;
 RT "Rapid Diagnostic Methods for food Borne Pathogens.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AJ537515; CAD68988.1; -; Genomic_DNA.
 DR SMR; Q5ZPY0; 1-276.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 FT NON_TER 1 1
 FT NON_TER 276 276
 SQ SEQUENCE 276 AA; 30213 MW; 2BE68939E84D6378 CRC64;

 Query Match 100.0%; Score 114; DB 2; Length 276;
 Best Local Similarity 100.0%; Pred. No. 7e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 CHHHASRVARMASDEFPSMC 20
 |||||||
 Db 233 CHHHASRVARMASDEFPSMC 252

RESULT 12
 Q7WZI8_ECO57
 ID Q7WZI8_ECO57 PRELIMINARY; PRT; 313 AA.
 AC Q7WZI8;
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2003, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Shiga toxin 1 variant A subunit.
 GN Name=stx1;
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AI2000/182;
RA Suzuki M.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; AB083043; BAC78637.1; -; Genomic_DNA.
DR HSSP; Q9FB12; 1DM0.
DR SMR; Q7WZI8; 23-312.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
SQ SEQUENCE 313 AA; 34640 MW; DDF7ABF58F30BD19 CRC64;

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Query Match          100.0%; Score 114; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHHHASRVARMASDEFPSMC 20
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Db      264 CHHHASRVARMASDEFPSMC 283

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RESULT 13
SLTA_BPH19
ID SLTA_BPH19 STANDARD; PRT; 315 AA.
AC P08026;
DT 01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1988, sequence version 1.
DT 07-FEB-2006, entry version 44.
DE Shiga-like toxin I subunit A precursor (EC 3.2.2.22) (Verotoxin 1
DE subunit A) (SLT-I) (rRNA N-glycosidase).
GN Name=sltA;
OS Bacteriophage H19B.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=69932;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=87260808; PubMed=3299365;
RA Calderwood S.B., Auclair F., Donohue-Rolfe A., Keusch G.T.,
RA Mekalanos J.J.;
RT "Nucleotide sequence of the Shiga-like toxin genes of Escherichia
RT coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4364-4368(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=87308020; PubMed=3040689;
RA de Grandis S., Ginsberg J., Toone M., Climie S., Friesen J.,
RA Brunton J.;
RT "Nucleotide sequence and promoter mapping of the Escherichia coli
RT Shiga-like toxin operon of bacteriophage H-19B.";
RL J. Bacteriol. 169:4313-4319(1987).
RN [3]
RP ACTIVE SITE.
RX MEDLINE=88190113; PubMed=3357883;
RA Hovde C.J., Calderwood S.B., Mekalanos J.J., Collier R.J.;
RT "Evidence that glutamic acid 167 is an active-site residue of Shiga
RT like toxin I.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2568-2572(1988).
CC -!- FUNCTION: The A subunit is responsible for inhibiting protein
CC synthesis through the catalytic inactivation of 60S ribosomal
CC subunits.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at
CC specific adenosine on the 28S rRNA.
CC -!- SUBUNIT: The Shiga-like toxins contain a single A subunit and
CC multiple copies of B subunit.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
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CC -----
DR EMBL; M16625; AAA98099.1; -; Genomic DNA.

DR EMBL; M17358; AAA32229.1; -; Genomic_DNA.
 DR PIR; A27052; XUBPH9.
 DR PIR; A53887; A53887.
 DR SMR; P08026; 23-312.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 22
 FT CHAIN 23 315 Shiga-like toxin I subunit A.
 FT /FTId=PRO_0000030791.
 FT ACT_SITE 189 189
 SQ SEQUENCE 315 AA; 34800 MW; 8B993DF7A8E58F30 CRC64;

 Query Match 100.0%; Score 114; DB 1; Length 315;
 Best Local Similarity 100.0%; Pred. No. 8.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHASRVARMASDEFPSMC 20
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 Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 14
 SLTA_BPH30
 ID SLTA_BPH30 STANDARD PRT; 315 AA.
 AC P10149;
 DT 01-JUL-1989, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUL-1989, sequence version 1.
 DT 07-FEB-2006, entry version 43.
 DE Shiga toxin A-chain precursor (EC 3.2.2.22) (rRNA N-glycosidase).
 GN Name=stxA;
 OS Bacteriophage H30.
 OC Viruses.
 OX NCBI_TaxID=12371;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=88139166; PubMed=2830229;
 RA Strockbine N.A., Jackson M.P., Sung L.M., Holmes R.K., O'Brien A.D.;
 RT "Cloning and sequencing of the genes for Shiga toxin from Shigella
 dysenteriae type 1.";
 RL J. Bacteriol. 170:1116-1122(1988).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Kozlov Y.V., Kabishev A.A., Fedchenko V.I., Bayev A.A.;
 RT "Cloning and primary structure of Shigella toxin genes.";
 RL Dokl. Biochem. 295:744-749(1987).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=89006281; PubMed=3049254; DOI=10.1016/0378-1119(88)90398-8;
 RA Kozlov Y.V., Kabishev A.A., Lukyanov E.V., Bayev A.A.;
 RT "The primary structure of the operons coding for Shigella dysenteriae
 toxin and temperature phage H30 shiga-like toxin.";
 RL Gene 67:213-221(1988).
 CC -!- FUNCTION: The A chain is responsible for inhibiting protein
 synthesis through the catalytic inactivation of 60S ribosomal
 subunits.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -!- SUBUNIT: Shiga toxin contains a single A-chain and five copies of
 B-chain.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.

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 CC -----
 DR EMBL; M19437; AAA98347.1; -; Genomic_DNA.
 DR EMBL; X07903; CAA30741.1; -; Genomic_DNA.
 DR EMBL; M24352; AAA26538.1; -; Genomic_DNA.
 DR EMBL; M23980; AAA72732.1; -; Genomic_DNA.
 DR SMR; P10149; 23-312.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 22

FT CHAIN 23 315 Shiga toxin A-chain.
 FT /FTId=PRO_0000030790.
 FT ACT_SITE 189 189 By similarity.
 FT CONFLICT 67 67 T -> S (in Ref. 3).
 FT CONFLICT 190 190 A -> P (in Ref. 2).
 SQ SEQUENCE 315 AA; 34814 MW; 8A423DF7ABF58F30 CRC64;

 Query Match 100.0%; Score 114; DB 1; Length 315;
 Best Local Similarity 100.0%; Pred. No. 8.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 CHHHASRVARMASDEFPSMC 20
 |||||||
 Db 264 CHHHASRVARMASDEFPSMC 283

RESULT 15
Q5MBW7_9CAUD
 ID Q5MBW7_9CAUD PRELIMINARY; PRT; 315 AA.
 AC Q5MBW7;
 DT 01-FEB-2005, integrated into UniProtKB/TrEMBL.
 DT 01-FEB-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE StxA1.
 GN Name=stxA1;
 OS Stx1-converting phage phi-O153.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC Lambda-like viruses; unclassified Lambda-like viruses.
 OX NCBI_TaxID=305853;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Karalius B.J., Butterton J.R.;
 RT "Nucleotide sequence of stx region of Stx1-producing rabbit E. coli
 strain O153:H-.";
 RL Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AY838795; AAW21758.1; -; Genomic_DNA.
 DR SMR; Q5MBW7; 23-312.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Protein synthesis inhibitor; Toxin.
 SQ SEQUENCE 315 AA; 34814 MW; 8A423DF7ABF58F30 CRC64;

 Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 8.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 CHHHASRVARMASDEFPSMC 20
 |||||||
 Db 264 CHHHASRVARMASDEFPSMC 283

Search completed: July 20, 2006, 09:53:06
 Job time : 21.8035 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 57.rag.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:35:59 ; Search time 16.1993 Seconds
(without alignments)
564.490 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSGQAGAAASESLFISHAY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as
7: geneseqp2003bs
8: geneseqp2004s:
9: geneseqp2005s:
10: geneseqp2006s

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						Description
	No.	Score	Match	Length	DB	ID	
1	100	100.0	20	2	AAR37301		Aar37301 Rabbit Mu
2	99	99.0	153	5	ABP42706		Abp42706 Human ova
3	99	99.0	363	2	AAY07116		Aay07116 Lung canc
4	99	99.0	364	2	AAY06992		Aay06992 Glycolyt
5	99	99.0	364	7	ADF76857		Adf76857 Novel hum
6	99	99.0	364	7	ADJ68731		Adj68731 Human hea
7	99	99.0	364	8	ADE77178		Adet77178 Human pro

8	99	99.0	364	8	ADIO2918	Adi02918 Human fru
9	99	99.0	364	8	ADQ76754	Adq76754 Human fru
10	99	99.0	364	8	ABM81754	Abm81754 Tumour-as
11	99	99.0	364	8	ADU46860	Adu46860 Aldolase
12	99	99.0	364	9	ADX05876	Adx05876 Cyclin-de
13	99	99.0	364	9	ADZ70640	Adz70640 Human pro
14	99	99.0	364	9	ADZ70327	Adz70327 Human pro
15	99	99.0	364	10	AEF21053	Aef21053 human ado
16	99	99.0	364	10	AEF41979	Aef41979 Fructose-
17	97	97.0	22	9	ADV50900	Adv50900 Murine br
18	97	97.0	364	7	ADB79827	Adb79827 Rat aldol
19	95	95.0	31	3	AAB44017	Aab44017 Human can
20	95	95.0	364	10	AEE88055	Aee88055 Human pro
21	68	68.0	363	9	ADW08677	Adw08677 Human pro
22	68	68.0	364	5	ABP65148	Abp65148 Hypoxia-r
23	68	68.0	364	7	ADJ68292	Adj68292 Human hea
24	68	68.0	364	8	ADL12661	Adl12661 Human ste
25	68	68.0	364	10	AEF21055	Aef21055 human ado
26	68	68.0	364	10	AEF27175	Aef27175 Human ald
27	68	68.0	364	10	AEF41981	Aef41981 Fructose-
28	61	61.0	365	8	ADN23270	Adn23270 Bacterial
29	55.5	55.5	361	4	ABB66969	Abb66969 Drosophil
30	52	52.0	366	8	ADN23082	Adn23082 Bacterial
31	51	51.0	371	8	ADY10167	Ady10167 Plant ful
32	50.5	50.5	215	8	ABO60233	Abo60233 Human gen
33	50.5	50.5	836	7	ABR83671	Abr83671 Human bK1
34	50.5	50.5	836	7	ADM05015	Adm05015 Human pro
35	50.5	50.5	836	8	ADO85827	Ado85827 Different
36	50.5	50.5	836	9	AEC87945	Aec87945 Human cDN
37	48	48.0	1772	8	ADR12606	Adr12606 Gene vacc
38	47	47.0	1223	4	ABB63399	Abb63399 Drosophil
39	46	46.0	9	8	ADN63558	Adn63558 HLA bindi
40	46	46.0	9	8	ADN64270	Adn64270 HLA bindi
41	46	46.0	132	6	ABP96323	Abp96323 Human AGE
42	46	46.0	170	6	ABU01993	Abu01993 S. pneumo
43	46	46.0	170	8	ADK46838	Adk46838 Streptoco
44	46	46.0	171	8	ADR95229	Adr95229 Novel S.
45	46	46.0	171	9	AEA59099	Aea59099 Streptoco

ALIGNMENTS

RESULT 1
AAR37301
ID AAR37301 standard; protein; 20 AA.
XX
AC AAR37301;
XX
DT 25-MAR-2003 (revised)
DT 13-SEP-1993 (first entry)
XX
DE Rabbit Muscle aldolase peptide segment.
XX
KW Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;
KW autoimmune disease; cell killing; toxin; human engineered antibody;
KW variable region; light chain; cell targetting; chimeric antibody; RMA;
KW linker.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT Cleavage-site 1..20
FT /note= "contains several potential cathepsin cleavage
sites"
XX
PN WO9309130-A1.
XX
PD 13-MAY-1993.
XX
PF 04-NOV-1992; 92WO-US009487.
XX
PR 04-NOV-1991; 91US-00787567.
PR 19-JUN-1992; 92US-00901707.
XX
PA (XOMA) XOMA CORP.

XX
PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;
XX
DR WPI; 1993-167617/20.
XX
PT Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo.
XX
PS Example 10; Page 115; 163pp; English.
XX
CC The invention covers analogues of the plant type I RIP gelonin which have a non-naturally occurring Cys residue in a position which enables the analogue to be conjugated via a disulphide linkage to a molecule which specifically binds to a target cell. Pref. target-cell binding molecules are antibodies or their fragments, esp. human engineered H65 antibody fragments. Fusion constructs were assembled that included a natural sequence gelonin gene fused to an H65 truncated heavy chain gene or an H65 light chain (kappa) gene. A DNA linker encoding a peptide segment of the rabbit muscle aldolase was inserted between the gelonin gene and the Ab gene. The resulting immunoconjugates can be used as cytotoxic therapeutic agents. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
||| ||| ||| ||| ||| ||| |||
Db 1 PSGQAGAAASESLFISHAY 20

RESULT 2
ABP42706
ID ABP42706 standard; protein; 153 AA.
XX
AC ABP42706;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HOPKN14, SEQ ID NO:3838.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
XX
OS Homo sapiens.
XX
PN WO200200677-A1.
XX
PD 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US018569.
XX
PR 07-JUN-2000; 2000US-0209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
DR N-PSDB; ABQ55783.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.

XX
PS Claim 11; SEQ ID NO 3838; 2922pp; English.
XX
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://wipo.int/pub/published_pct_sequences
XX
SQ Sequence 153 AA;

Query Match 99.0%; Score 99; DB 5; Length 153;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||:|||||:
Db 134 PSGQAGAAASESLFVSNHAY 153

RESULT 3
AAY07116
ID AAY07116 standard; protein; 363 AA.
XX
AC AAY07116;
XX
DT 02-JUL-1999 (first entry)
XX
DE Lung cancer associated antigen precursor sequence.
XX
KW Cancer associated antigen; diagnosis; research; treatment; human;
KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
KW prostate cancer.
XX
OS Homo sapiens.
XX
PN WO9904265-A2.
XX
PD 28-JAN-1999.
XX
PF 15-JUL-1998; 98WO-US014679.
XX
PR 17-JUL-1997; 97US-00896164.
PR 10-OCT-1997; 97US-0061599P.
PR 10-OCT-1997; 97US-0061765P.
PR 10-OCT-1997; 97US-00948705.
PR 11-OCT-1997; 97GB-00021697.
PR 22-JUN-1998; 98US-00102322.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;

PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
XX
DR WPI; 1999-132448/11.
XX
PT New isolated cancer associated nucleic acids and polypeptides - isolated
PT using sera from cancer patients, used to develop products for the
PT diagnosis, monitoring or treatment of cancers.
XX
PS Disclosure; Page 733-734; 787pp; English.
XX
CC The invention relates to a method for diagnosing a disorder characterised
CC by expression of a human cancer associated antigen precursor coded for by
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC biological sample isolated from a subject with an agent that specifically
CC binds to the NAM, an expression product or a fragment of an expression
CC product complexed with an HLA molecule; and (b) determining the
CC interaction between the agent and the NAM or the expression product as a
CC determination of the disorder. The products and methods can be used in
CC the diagnosis, monitoring, research, or treatment of conditions
CC characterised by the expression of various cancer associated antigens.
CC The invention provides nucleic acid sequences and encoded polypeptides
CC which are cancer associated antigen precursors expressed in human breast
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
CC lung cancer
XX
SQ Sequence 363 AA;

Query Match 99.0%; Score 99; DB 2; Length 363;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||:|||||:
Db 344 PSGQAGAAASESLFVSNHAY 363

RESULT 4
AAY06992
ID AAY06992 standard; protein; 364 AA.
XX
AC AAY06992;
XX
DT 02-JUL-1999 (first entry)
XX
DE Glycolytic enzyme aldolase A.
XX
KW Cancer associated antigen; diagnosis; research; treatment; human;
KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
KW prostate cancer.
XX
OS Homo sapiens.
XX
PN WO9904265-A2.
XX
PD 28-JAN-1999.
XX
PF 15-JUL-1998; 98WO-US014679.
XX
PR 17-JUL-1997; 97US-00896164.
PR 10-OCT-1997; 97US-0061599P.
PR 10-OCT-1997; 97US-0061765P.
PR 10-OCT-1997; 97US-00948705.
PR 11-OCT-1997; 97GB-00021697.
PR 22-JUN-1998; 98US-00102322.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
XX
DR WPI; 1999-132448/11.
DR N-PSDB; AAX40193.
XX
PT New isolated cancer associated nucleic acids and polypeptides - isolated
PT using sera from cancer patients, used to develop products for the
PT diagnosis, monitoring or treatment of cancers.

XX
PS Example 8; Page 769-770; 787pp; English.
XX
CC The invention relates to a method for diagnosing a disorder characterised
CC by expression of a human cancer associated antigen precursor coded for by
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC biological sample isolated from a subject with an agent that specifically
binds to the NAM, an expression product or a fragment of an expression
CC product complexed with an HLA molecule; and (b) determining the
CC interaction between the agent and the NAM or the expression product as a
determination of the disorder. The products and methods can be used in
CC the diagnosis, monitoring, research, or treatment of conditions
characterised by the expression of various cancer associated antigens.
CC The invention provides nucleic acid sequences and encoded polypeptides
CC which are cancer associated antigen precursors expressed in human breast
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
CC lung cancer
XX
SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 2; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||:|||||
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 5
AD76857
ID ADF76857 standard; protein; 364 AA.
XX
AC ADF76857;
XX
DT 26-FEB-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein SeqID 532.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neuropeptide; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
PN WO2003072035-A2.
XX
PD 04-SEP-2003.
XX
PF 21-FEB-2003; 2003WO-US005241.
XX
PR 22-FEB-2002; 2002US-0359461P.
XX
PA (GETH) GENENTECH INC.
XX
PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
PI Williams PM, Wood WI, Wu TD;
XX
DR WPI; 2003-721702/68.
DR N-PSDB; ADF76856.
XX
PT New PRO polypeptides, useful for diagnosing and treating an immune
PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
PT diabetes mellitus.
XX
PS Claim 10; SEQ ID NO 532; 918pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information

CC is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the invention.

XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 7; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHNAY 20
|||||||:||||:|||||
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 6

ADJ68731

ID ADJ68731 standard; protein; 364 AA.

XX

AC ADJ68731;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human heat mitochondrial protein as a therapeutic target SeqID537.

XX

KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.

XX

OS Homo sapiens.

XX

PN WO2003087768-A2.

XX

PD 23-OCT-2003.

XX

PF 04-APR-2003; 2003WO-US010870.

XX

PR 12-APR-2002; 2002US-0372843P.

PR 17-JUN-2002; 2002US-0389987P.

PR 20-SEP-2002; 2002US-0412418P.

XX

PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.

XX

PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;

XX

DR WPI; 2003-845369/78.

XX

PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.

XX

PS Claim 1; SEQ ID NO 537; 180pp; English.

XX

CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are

CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 7; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||:|||||
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 7
ADE77178
ID ADE77178 standard; protein; 364 AA.
XX
AC ADE77178;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human protein expressed in a liver disorder #87.
XX
KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
KW tumour; liver; inflammatory disorder; immune response disorder;
KW high-throughput screening; differential gene expression; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003108871-A1.
XX
PD 12-JUN-2003.
XX
PF 30-JUL-2001; 2001US-00919039.
XX
PR 28-JUL-2000; 2000US-0222113P.
XX
PA (KASE/) KASER M R.
XX
PI Kaser MR;
XX
DR WPI; 2004-031227/03.
DR N-PSDB; ADE77177.
XX
PT Composition comprising several cDNAs that are differentially expressed in
PT treated human C3A liver cell cultures, useful for treating liver
PT disorders.
XX
PS Claim 1: SEQ ID NO 343; 41pp; English.
XX
CC The invention relates to a composition comprising several cDNAs that are
CC differentially expressed in a liver disorder. The composition is useful
CC for treating liver disorder such as hyperlipidaemia, hypertension, type
CC II diabetes, tumours of the liver and disorders of the inflammatory and
CC immune response. The composition is useful for a high-throughput method
CC of screening several molecules or compounds to identify a ligand which
CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
CC high-throughput method for using a protein to screen several molecules or
CC compounds to identify at least one ligand which specifically binds the
CC protein which involves combining the protein encoded by the cDNA with
CC several of molecules or compounds under conditions to allow specific
CC binding, and detecting specific binding between the protein and a
CC molecule or compound, therefore identifying a ligand which specifically
CC binds the protein. The composition is useful for detecting and
CC quantifying differential gene expression, can be used in gene therapy, to
CC formulate prognosis and to design a treatment regimen and to monitor the

CC efficacy of treatment. The present sequence represents the amino acid
CC sequence of a protein encoded by a cDNA differentially expressed in a
CC liver disorder.

XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||||||:|||||:
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 8

ADIO2918

ID ADI02918 standard; protein; 364 AA.

XX

AC ADI02918;

XX

DT 22-APR-2004 (first entry)

XX

DE Human fructose-bisphosphate aldolase.

XX

KW gene database preparation; cDNA microarray; human;
KW fructose-bisphosphate aldolase; GP2; enzyme.

XX

OS Homo sapiens.

XX

PN JP2004005319-A.

XX

PD 08-JAN-2004.

XX

PF 10-JUN-2002; 2002JP-00168894.

XX

PR 24-APR-2002; 2002JP-00123176.

XX

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.

XX

DR WPI; 2004-113174/12.

DR N-PSDB; ADI02917.

XX

PT Gene database production method for microarray preparation, comprises
PT searching homology of a candidate sequence determined by a primer probe

PT designing unit, for a matching candidate sequence.

XX

PS Disclosure; Fig 9; 33pp; Japanese.

XX

CC The invention relates to a method for preparing a gene database. The
CC method comprises a search unit searching homology of a candidate sequence
CC determined by a primer probe designing unit, for determining homologous
CC presence or absence of a determined candidate sequence. The method of the
CC invention is useful for the preparation of a microarray, such as a cDNA
CC microarray. The present amino acid sequence represents a human fructose-
CC bisphosphate aldolase.

XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||||||:|||||:
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 9

ADQ76754

ID ADQ76754 standard; protein; 364 AA.

XX

AC ADQ76754;

XX

DT 07-OCT-2004 (first entry)

XX DE Human fructose bisphosphate aldolase A, target for anti-HIV agent.
XX KW Human; fructose bisphosphate aldolase A; enzyme;
KW human immunodeficiency virus; HIV; anti-HIV; virucide.
XX OS Homo sapiens.
XX PN WO2004061088-A2.
XX PD 22-JUL-2004.
XX PF 30-DEC-2003; 2003WO-US041790.
XX PR 30-DEC-2002; 2002US-0436936P.
XX PA (PPDP-) PPD DEV LP.
XX PI Dunn SJ;
XX DR WPI; 2004-534379/51.
DR N-PSDB; ADQ76753.
XX PT Use of an inhibitor of a member of a biological pathway for inhibiting,
PT suppressing, treating, or preventing human immunodeficiency virus (HIV)
PT infection.
XX PS Claim 1; SEQ ID NO 22; 143pp; English.
XX CC The present sequence is that of human fructose bisphosphate aldolase A
CC (ALDOA), which has been identified as a cellular target for HIV
CC inhibition. The invention relates to methods for identifying human
CC cellular genes that encode products that are necessary for productive HIV
CC infection for use as targets in the design of therapeutic agents for
CC suppressing HIV infection. The invention also includes methods for
CC identifying biological pathways comprising the products of such cellular
CC genes, as well as substrates and metabolic products of these pathways,
CC and methods for identifying additional human cellular genes that encode
CC products comprising other members of such pathways for use as targets in
CC the design of therapeutic agents for suppressing HIV infection. It also
CC relates to methods for identifying protective compounds that inhibit HIV
CC infection and to the use of such compounds in the treatment or prevention
CC of HIV. The compounds include chemical compounds such as small molecule
CC inhibitors or substrate compounds such as products of chemical
CC combinatorial libraries, or biological compounds including peptides,
CC antisense molecules and antibodies. In one embodiment of the invention,
CC the target gene encodes a target product that is a member of the
CC glycolysis pathway of the host cell. Random fragment expression libraries
CC were constructed from mRNA isolated from HL-60 and HeLa cells, and from
CC phytohaemagglutinin-stimulated peripheral blood mononuclear cells (PBMC).
CC These were used for the isolation and identification of human cell-
CC derived genetic suppressor elements (GSEs) exhibiting HIV suppressive
CC activity. The human cellular genes from which these GSEs were derived
CC were identified, and included the ALDOA gene from a PBMC library.
XX SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||:||||:|||||
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 10
ABM81754
ID ABM81754 standard; protein; 364 AA.
XX AC ABM81754;
XX DT 18-NOV-2004 (first entry)
XX DE Tumour-associated antigenic target (TAT) polypeptide PRO69617, SEQ:4521.
XX

KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
DR N-PSDB; ACN40010.
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 4521; 7273pp; English.
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||:|||||:
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 11
ADU46860
ID ADU46860 standard; protein; 364 AA.
XX
AC ADU46860;
XX
DT 27-JAN-2005 (first entry)
XX
DE Aldolase A fructose bisphosphate.
XX
KW mammal; breast; cancer; increased risk; prognosis; biomarker.
XX

OS Homo sapiens.
XX
PN WO2004097030-A2.
XX
PD 11-NOV-2004.
XX
PF 28-APR-2004; 2004WO-US013076.
XX
PR 28-APR-2003; 2003US-0466084P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Bergh J, Pawitan Y, Hall P, Amler LC, Han X, Huang F, Shaw P;
XX
DR WPI; 2004-804769/79.
DR N-PSDB; ADU46827.
DR GENBANK; NP_000025.
XX
PT Identifying a mammal at increased risk for developing breast cancer by
PT correlating the level of at least one biomarker with a baseline level and
PT identifying a mammal at increased risk for developing breast cancer based
PT on the correlation.
XX
PS Claim 1; SEQ ID NO 50; 150pp; English.
XX
CC This sequence represents the aldolase A fructose bisphosphate. This
CC sequence may be used in the method of the invention for identifying a
CC mammal at increased risk for developing breast cancer. The method
CC comprises correlating the level of at least one biomarker with a baseline
CC level and identifying a mammal at increased risk for developing breast
CC cancer based on the correlation. The method is useful for identifying a
CC mammal at increased risk for developing breast cancer. Preferably, it is
CC useful for prognosing breast cancer in a mammal and for identifying
CC breast cancer in a mammal, by measuring the level of a biomarker such as
CC a protein or an mRNA transcript of the biomarker.
XX
SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||:|||||:
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 12
ADX05876
ID ADX05876 standard; protein; 364 AA.
XX
AC ADX05876;
XX
DT 21-APR-2005 (first entry)
XX
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 441.
XX
KW cytostatic; cyclin-dependent kinase; cdk; biomarker.
XX
OS Homo sapiens.
XX
PN WO2005012875-A2.
XX
PD 10-FEB-2005.
XX
PF 29-JUL-2004; 2004WO-US024424.
XX
PR 29-JUL-2003; 2003US-0490890P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
DR WPI; 2005-163068/17.
DR N-PSDB; ADX05875.

XX
PT Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.
XX
PS Claim 5; SEQ ID NO 441; 141pp; English.
XX
CC This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-
CC oxazolyl)methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
CC sequence represents a biomarker used in the method of the invention.
XX
SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 9; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||:|||||
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 13
ADZ70640
ID ADZ70640 standard; protein; 364 AA.
XX
AC ADZ70640;
XX
DT 30-JUN-2005 (first entry)
XX
DE Human protein from lung cancer marker gene ALDOA, SEQ ID 325.
XX
KW Tumor marker; lung tumor; cytostatic; neoplasm; expression;
KW DNA microarray.
XX
OS Homo sapiens.
XX
PN WO2005032495-A2.
XX
PD 14-APR-2005.
XX
PF 01-OCT-2004; 2004WO-US034163.
XX
PR 03-OCT-2003; 2003US-0508355P.
XX
PA (FARB) BAYER PHARM CORP.
XX
PI Taylor I, Pauloski NR, Bigwood D;
XX
DR WPI; 2005-285325/29.
DR N-PSDB; ADZ70639.
XX
PT Providing a patient diagnosis for lung cancer comprises comparing the
PT level of expression of genes or gene products in a biological sample from
PT the patient with that from a normal individual.
XX
PS Claim 3; SEQ ID NO 325; 60pp; English.
XX
CC The invention relates to providing a patient diagnosis for lung cancer
CC comprising comparing the level of expression of genes or gene products in

CC a biological sample from the patient with the level of expression of
CC genes or gene products in a biological sample from a normal individual.
CC Also included are distinguishing between normal and disease tissues,
CC monitoring the response of a patient being treated for lung cancer by
CC administering an anti-cancer agent, identifying a compound useful for the
CC treatment of lung cancer and an array for distinguishing between normal
CC and disease tissues (comprising 2 or more probes corresponding to 2 or
CC more genes selected from any of the 200 nucleotide sequences given in the
CC specification, or 2 or more polypeptides comprising any of the 200 amino
CC acid sequences given in the specification). In providing a patient
CC diagnosis for lung cancer, one or more genes are selected from any of the
CC 200 nucleotide sequences as mentioned in the specification, or one or
CC more gene products are polypeptides selected from any of the 20 amino
CC acid sequences mentioned in the specification. The methods are useful for
CC detecting and treating lung cancer. These may also be used for designing,
CC identifying and optimizing therapeutics for cancer. The present sequence
CC represents a protein from one of the 200 lung cancer marker genes. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 9; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20
|||:|||||:|||||
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 14

ADZ70327

ID ADZ70327 standard; protein; 364 AA.

XX

AC ADZ70327;

XX

DT 30-JUN-2005 (first entry)

XX

DE Human protein from lung cancer marker gene ALDOA, SEQ ID 12.

XX

KW Tumor marker; lung tumor; cytostatic; neoplasm; expression;
KW DNA microarray.

XX

OS Homo sapiens.

XX

PN WO2005032495-A2.

XX

PD 14-APR-2005.

XX

PF 01-OCT-2004; 2004WO-US034163.

XX

PR 03-OCT-2003; 2003US-0508355P.

XX

PA (FARB) BAYER PHARM CORP.

XX

PI Taylor I, Pauloski NR, Bigwood D;

XX

DR WPI; 2005-285325/29.

DR N-PSDB; ADZ70326.

XX

PT Providing a patient diagnosis for lung cancer comprises comparing the
PT level of expression of genes or gene products in a biological sample from
PT the patient with that from a normal individual.

XX

PS Claim 3; SEQ ID NO 12; 60pp; English.

XX

CC The invention relates to providing a patient diagnosis for lung cancer
CC comprising comparing the level of expression of genes or gene products in
CC a biological sample from the patient with the level of expression of
CC genes or gene products in a biological sample from a normal individual.
CC Also included are distinguishing between normal and disease tissues,
CC monitoring the response of a patient being treated for lung cancer by
CC administering an anti-cancer agent, identifying a compound useful for the
CC treatment of lung cancer and an array for distinguishing between normal

CC and disease tissues (comprising 2 or more probes corresponding to 2 or
CC more genes selected from any of the 200 nucleotide sequences given in the
CC specification, or 2 or more polypeptides comprising any of the 200 amino
CC acid sequences given in the specification). In providing a patient
CC diagnosis for lung cancer, one or more genes are selected from any of the 200
CC nucleotide sequences as mentioned in the specification, or one or
CC more gene products are polypeptides selected from any of the 20 amino
CC acid sequences mentioned in the specification. The methods are useful for
CC detecting and treating lung cancer. These may also be used for designing,
CC identifying and optimizing therapeutics for cancer. The present sequence
CC represents a protein from one of the 200 lung cancer marker genes. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 9; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20
|||:|||||:|||||
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 15

AEF21053

ID AEF21053 standard; protein; 364 AA.

XX

AC AEF21053;

XX

DT 09-MAR-2006 (first entry)

XX

DE human adolase A SEQ ID NO 1.

XX

KW diagnosis; protein interaction; retinal neovascularization;
KW ophthalmological; ocular disease; diabetic retinopathy; antidiabetic;
KW cardiovascular disease; antiinflammatory; edema;
KW age related macular degeneration; adolase A; enzyme.

XX

OS Homo sapiens.

XX

PN WO2006004249-A1.

XX

PD 12-JAN-2006.

XX

PF 14-MAR-2005; 2005WO-KR000722.

XX

PR 06-JUL-2004; 2004KR-00052385.

XX

PA (KUHN-) KUHNIL PHARM CO LTD.

XX

PI Cho Y, Ahn B, Yoo W, Kwon O;

XX

DR WPI; 2006-090524/09.

DR REFSEQ; NP_908932.

XX

PT Composition useful for diagnosing retinal vascular disease, comprises
PT aldolase such as aldolase A, aldolase B and aldolase C.

XX

PS Claim 2; SEQ ID NO 1; 45pp; English.

XX

CC The invention describes a composition (I) for diagnosing retinal vascular
CC disease, comprising an aldolase. Also described are: a kit (II) for
CC diagnosing retinal vascular disease, comprising an aldolase; and
CC diagnosing (M1) retinal vascular disease, comprising: bringing a
CC biological sample into contact with an aldolase; and detecting formed
CC antigen-autoantibody complexes. (I) is useful for diagnosing retinal
CC vascular disease, which is chosen from diabetic retinopathy, retinal
CC edema and age-related macular degeneration. (I) enables simple, rapid,
CC accurate and cost-effective diagnosis of the retinal vascular disease
CC e.g. diabetic retinopathy. This is the amino acid sequence of human
CC adolase A.

XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 10; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PSGQAGAAASESLFISHAY 20
|||||||:|||||
Db 345 PSGQAGAAASESLFVSNHAY 364

Search completed: July 20, 2006, 09:43:40
Job time : 19.1993 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 57.rai.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:37:31 ; Search time 2.69373 Seconds
(without alignments)
649.885 Million cell updates/sec

Title: US-10-717-243-57
Perfect score: 100
Sequence: 1 PSGQAGAAASESLFISNHAY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /EMC_Celerra_SID3/ptodata/2/iaa/5_COMB.pep:
2: /EMC_Celerra_SID3/ptodata/2/iaa/6_COMB.pep:
3: /EMC_Celerra_SID3/ptodata/2/iaa/7_COMB.pep:
4: /EMC_Celerra_SID3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SID3/ptodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SID3/ptodata/2/iaa/RE_COMB.pep:
7: /EMC_Celerra_SID3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	100	100.0	20	1	US-07-988-430-59	Sequence 59, Appl
2	100	100.0	20	1	US-08-425-336-57	Sequence 57, Appl
3	100	100.0	20	1	US-08-488-113B-57	Sequence 57, Appl
4	100	100.0	20	1	US-08-477-484B-57	Sequence 57, Appl
5	100	100.0	20	1	US-08-646-360-57	Sequence 57, Appl
6	100	100.0	20	2	US-08-839-765-57	Sequence 57, Appl
7	100	100.0	20	2	US-09-136-389-57	Sequence 57, Appl
8	100	100.0	20	2	US-09-610-838-57	Sequence 57, Appl
9	100	100.0	20	2	US-09-711-485-57	Sequence 57, Appl
10	100	100.0	20	5	PCT-US92-09487-59	Sequence 59, Appl

11	99	99.0	364	2	US-09-919-039-343	Sequence 343, Ap
12	99	99.0	419	2	US-09-949-016-8781	Sequence 8781, Ap
13	68	68.0	364	2	US-09-976-594-390	Sequence 390, Ap
14	46	46.0	170	2	US-09-583-110-3353	Sequence 3353, Ap
15	46	46.0	171	2	US-09-107-433-3864	Sequence 3864, Ap
16	46	46.0	377	2	US-09-949-016-9474	Sequence 9474, Ap
17	45	45.0	659	2	US-09-228-986-75	Sequence 75, Appl
18	45	45.0	659	2	US-10-101-464A-75	Sequence 75, Appl
19	45	45.0	736	2	US-09-252-991A-21498	Sequence 21498, A
20	44	44.0	176	2	US-09-252-991A-29061	Sequence 29061, A
21	44	44.0	863	2	US-09-252-991A-21831	Sequence 21831, A
22	43	43.0	200	2	US-09-540-236-3005	Sequence 3005, Ap
23	43	43.0	253	2	US-09-530-058-6	Sequence 6, Appli
24	43	43.0	593	2	US-09-252-991A-23340	Sequence 23340, A
25	43	43.0	697	2	US-09-949-016-9660	Sequence 9660, Ap
26	42	42.0	277	2	US-09-710-279-2802	Sequence 2802, Ap
27	42	42.0	278	2	US-09-252-991A-26039	Sequence 26039, A
28	42	42.0	461	2	US-09-122-210-2	Sequence 2, Appli
29	42	42.0	461	2	US-09-443-681-2	Sequence 2, Appli
30	42	42.0	626	2	US-09-949-016-6776	Sequence 6776, Ap
31	42	42.0	732	2	US-09-134-000C-6359	Sequence 6359, Ap
32	42	42.0	1017	2	US-09-134-001C-3542	Sequence 3542, Ap
33	42	42.0	1027	2	US-09-710-279-3106	Sequence 3106, Ap
34	41	41.0	139	2	US-09-270-767-36667	Sequence 36667, A
35	41	41.0	139	2	US-09-270-767-51884	Sequence 51884, A
36	41	41.0	244	2	US-09-068-804-38	Sequence 38, Appl
37	40	40.0	154	1	US-08-449-644-7	Sequence 7, Appli
38	40	40.0	154	1	US-08-087-244A-7	Sequence 7, Appli
39	40	40.0	291	2	US-10-094-749-2213	Sequence 2213, Ap
40	40	40.0	304	2	US-09-270-767-32299	Sequence 32299, A
41	40	40.0	304	2	US-09-270-767-47516	Sequence 47516, A
42	40	40.0	426	2	US-09-489-039A-8551	Sequence 8551, Ap
43	40	40.0	449	4	US-09-041-075A-21	Sequence 21, Appl
44	40	40.0	498	2	US-09-489-039A-13251	Sequence 13251, A
45	40	40.0	708	2	US-09-328-352-6131	Sequence 6131, Ap

ALIGNMENTS

RESULT 1
 US-07-988-430-59
; Sequence 59, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-988-430-59

Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
||| ||| ||| ||| ||| ||| |||
Db 1 PSGQAGAAASESLFISHAY 20

RESULT 2
US-08-425-336-57
; Sequence 57, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-425-336-57

Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
Db 1 PSGQAGAAASESLFISHAY 20

RESULT 3
US-08-488-113B-57
: Sequence 57, Application US/08488113B
: Patent No. 5744580
: GENERAL INFORMATION:
: APPLICANT: Better, Marc D.
: APPLICANT: Carroll, Stephen F.
: APPLICANT: Studnika, Gary M.
: TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
: TITLE OF INVENTION: Proteins
: NUMBER OF SEQUENCES: 169
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McAndrews, Held & Malloy, Ltd.
: STREET: 500 West Madison Street, 34th floor
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60661
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/488,113B
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/425,336
: FILING DATE: 18-APR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/064,691
: FILING DATE: 12-MAY-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/988,430
: FILING DATE: 09-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/901,707
: FILING DATE: 19-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/787,567
: FILING DATE: 04-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: McNicholas, Janet M.
: REGISTRATION NUMBER: 32,918
: REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/707-8889
: TELEFAX: 312/707-9155
: TELEX: 650 388-1248
: INFORMATION FOR SEQ ID NO: 57:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 20 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-488-113B-57

Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
Db 1 PSGQAGAAASESLFISHAY 20

RESULT 4
US-08-477-484B-57
; Sequence 57, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-484B-57

Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
Db 1 PSGQAGAAASESLFISHAY 20

RESULT 5
US-08-646-360-57
; Sequence 57, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-646-360-57

Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
| | | | | | | | | | | | | | | |
Db 1 PSGQAGAAASESLFISHAY 20

RESULT 6
US-08-839-765-57
; Sequence 57, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA

; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-839-765-57

Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
Db 1 PSGQAGAAASESLFISHAY 20

RESULT 7
US-09-136-389-57
; Sequence 57, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-136-389-57

Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||||||||||||||||||
Db 1 PSGQAGAAASESLFISHAY 20

RESULT 8
US-09-610-838-57
; Sequence 57, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348

; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-610-838-57 .

Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
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Db 1 PSGQAGAAASESLFISHAY 20

RESULT 9
US-09-711-485-57
; Sequence 57, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-711-485-57

Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
Db 1 PSGQAGAAASESLFISHAY 20

RESULT 10
PCT-US92-09487-59
; Sequence 59, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids

; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US92-09487-59

Query Match 100.0%; Score 100; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PSGQAGAAASESLFISNHAY 20
Db 1 PSGQAGAAASESLFISNHAY 20

RESULT 11
US-09-919-039-343
; Sequence 343, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 343
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 2706606CD1
US-09-919-039-343

Query Match 99.0%; Score 99; DB 2; Length 364;
Best Local Similarity 95.0%; Pred. No. 1.1e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PSGQAGAAASESLFISNHAY 20
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 12
US-09-949-016-8781
; Sequence 8781, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8781
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8781

Query Match 99.0%; Score 99; DB 2; Length 419;
Best Local Similarity 95.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PSGQAGAAASESLFISNHAY 20

|||||:|||||:|||||
Db 400 PSGQAGAAASESLFVSNHAY 419

RESULT 13
US-09-976-594-390
; Sequence 390, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 390
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 2705321CD1
US-09-976-594-390

Query Match 68.0%; Score 68; DB 2; Length 364;
Best Local Similarity 63.2%; Pred. No. 0.0022;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SGQAGAAASESLFISNHAY 20
||: | ||::||:||:|||||
Db 346 SGEDGGAAAQSLYIANHAY 364

RESULT 14
US-09-583-110-3353
; Sequence 3353, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3353
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3353

Query Match 46.0%; Score 46; DB 2; Length 170;
Best Local Similarity 52.4%; Pred. No. 5;
Matches 11; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 2 SGQAGAAASE--SLFISNHAY 20
||||| | | |||| |
Db 42 SGQAGVVCQEPADFFESNHLY 62

RESULT 15
US-09-107-433-3864
; Sequence 3864, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER:
; OPERATING SYSTEM:
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3864:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1..171
; SEQUENCE DESCRIPTION: SEQ ID NO: 3864:
US-09-107-433-3864

Query Match 46.0%; Score 46; DB 2; Length 171;
Best Local Similarity 52.4%; Pred. No. 5.1;
Matches 11; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 2 SGQAGAAASE--SLFISNHAY 20
Db 43 SGQAGVVCQEPADFFESNHLY 63

Search completed: July 20, 2006, 09:38:55
Job time : 3.69373 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 57.rapbm.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10717243 and Search Result us-10-717-243-57.rapbm.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:40:12 ; Search time 6.49446 Seconds
(without alignments)
1426.491 Million cell updates/sec

Title: US-10-717-243-57
Perfect score: 100
Sequence: 1 PSGQAGAAASESLFISNHAY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	100	100.0	20	4	US-10-127-890-57	Sequence 57, Appl
2	100	100.0	20	5	US-10-717-243-57	Sequence 57, Appl
3	99	99.0	153	4	US-10-264-049-3838	Sequence 3838, Ap
4	99	99.0	364	3	US-09-919-039-343	Sequence 343, App
5	99	99.0	364	4	US-10-408-765A-537	Sequence 537, App
6	99	99.0	364	5	US-10-370-715B-532	Sequence 532, App
7	97	97.0	364	4	US-10-205-219-67	Sequence 67, Appl
8	96	96.0	112	4	US-10-425-115-196160	Sequence 196160,
9	95	95.0	31	3	US-09-925-301-1462	Sequence 1462, Ap
10	68	68.0	363	5	US-10-878-556A-14	Sequence 14, Appl
11	68	68.0	364	4	US-10-170-385-259	Sequence 259, App

12	68	68.0	364	4	US-10-408-765A-98	Sequence 98, Appl
13	61	61.0	365	4	US-10-369-493-5923	Sequence 5923, Ap
14	55.5	55.5	361	4	US-10-108-605-255	Sequence 255, App
15	55.5	55.5	361	6	US-11-097-143-27699	Sequence 27699, A
16	52	52.0	366	4	US-10-369-493-5735	Sequence 5735, Ap
17	51	51.0	358	4	US-10-767-701-46629	Sequence 46629, A
18	51	51.0	361	4	US-10-425-115-269098	Sequence 269098,
19	51	51.0	371	4	US-10-425-114-65982	Sequence 65982, A
20	51	51.0	371	4	US-10-425-115-269100	Sequence 269100,
21	50.5	50.5	215	4	US-10-029-386-33867	Sequence 33867, A
22	50.5	50.5	836	4	US-10-108-260A-3700	Sequence 3700, Ap
23	47	47.0	1223	6	US-11-097-143-16989	Sequence 16989, A
24	46	46.0	9	5	US-10-530-061-870	Sequence 158, App
25	46	46.0	98	4	US-10-424-599-161041	Sequence 870, App
26	46	46.0	132	4	US-10-484-364-2	Sequence 161041,
27	46	46.0	170	5	US-10-472-928-3140	Sequence 2, Appli
28	46	46.0	171	5	US-10-617-320-3864	Sequence 3140, Ap
29	46	46.0	332	4	US-10-425-114-44042	Sequence 3864, Ap
30	46	46.0	355	4	US-10-425-114-44220	Sequence 44042, A
31	46	46.0	355	4	US-10-425-114-45677	Sequence 44220, A
32	46	46.0	358	4	US-10-424-599-222971	Sequence 45677, A
33	46	46.0	364	4	US-10-177-293-8	Sequence 222971,
34	46	46.0	372	4	US-10-425-114-43852	Sequence 8, Appli
35	46	46.0	372	4	US-10-425-114-44097	Sequence 43852, A
36	46	46.0	372	4	US-10-425-114-44837	Sequence 44097, A
37	46	46.0	375	4	US-10-425-114-45592	Sequence 44837, A
38	46	46.0	375	4	US-10-425-114-51423	Sequence 45592, A
39	46	46.0	375	4	US-10-425-114-55978	Sequence 51423, A
40	46	46.0	375	4	US-10-425-114-55981	Sequence 55978, A
41	46	46.0	392	4	US-10-437-963-151748	Sequence 55981, A
42	46	46.0	416	4	US-10-437-963-180885	Sequence 151748,
43	46	46.0	644	4	US-10-408-765A-1196	Sequence 180885,
44	46	46.0	902	4	US-10-029-386-32110	Sequence 1196, Ap
45	46	46.0				Sequence 32110, A

ALIGNMENTS

RESULT 1
 US-10-127-890-57
 ; Sequence 57, Application US/10127890
 ; Publication No. US20030166196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; Carroll, Stephen F.
 ; Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
 ; NUMBER OF SEQUENCES: 173
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/127,890
 ; FILING DATE: 23-Apr-2002
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/646,360
 ; FILING DATE: 13-MAY-1996
 ; APPLICATION NUMBER: PCT/US94/05348
 ; FILING DATE: 12-MAY-1994
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-127-890-57

Query Match 100.0%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
||| ||| ||| ||| ||| ||| |||
Db 1 PSGQAGAAASESLFISHAY 20

RESULT 2
US-10-717-243-57
; Sequence 57, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155

; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-717-243-57

Query Match 100.0%; Score 100; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
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Db 1 PSGQAGAAASESLFISHAY 20

RESULT 3

US-10-264-049-3838

; Sequence 3838, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3838
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-3838

Query Match 99.0%; Score 99; DB 4; Length 153;
Best Local Similarity 95.0%; Pred. No. 8.7e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
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Db 134 PSGQAGAAASESLFVSNHAY 153

RESULT 4

US-09-919-039-343

; Sequence 343, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 343
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 2706606CD1
US-09-919-039-343

Query Match 99.0%; Score 99; DB 3; Length 364;
Best Local Similarity 95.0%; Pred. No. 2.2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||||||:|||||
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 5
US-10-408-765A-537
; Sequence 537, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 537
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-537

Query Match 99.0%; Score 99; DB 4; Length 364;
Best Local Similarity 95.0%; Pred. No. 2.2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||||||:|||||
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 6
US-10-370-715B-532
; Sequence 532, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY,SARAH C.
; APPLICANT: CLARK,HILLARY
; APPLICANT: BRISDELL,HUNTE
; APPLICANT: JACKMAN,JANET
; APPLICANT: SCHOENFELD,JILL R.
; APPLICANT: WILLIAMS,P. MICKEY
; APPLICANT: WOOD,WILLIAM I.
; APPLICANT: WU,THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 532
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-532

Query Match 99.0%; Score 99; DB 5; Length 364;
Best Local Similarity 95.0%; Pred. No. 2.2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||||||:|||||
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 7

US-10-205-219-67
; Sequence 67, Application US/10205219
; Publication No. US20030138803A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018200
; CURRENT APPLICATION NUMBER: US/10/205,219
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Aldolase A

US-10-205-219-67

Query Match 97.0%; Score 97; DB 4; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.7e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
Db 345 PSGQSGAAASESLFISHAY 364

RESULT 8

US-10-425-115-196160
; Sequence 196160, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 196160
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(112)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_110484C.1.pep

US-10-425-115-196160

Query Match 96.0%; Score 96; DB 4; Length 112;
Best Local Similarity 95.0%; Pred. No. 1.9e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
Db 93 PSGQXGAAASESLFISHAY 112

RESULT 9

US-09-925-301-1462
; Sequence 1462, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1462
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (13)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1462

Query Match 95.0%; Score 95; DB 3; Length 31;
Best Local Similarity 90.0%; Pred. No. 6.8e-08;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
| :|||||:||||:|||||
Db 12 PXGQAGAAASESLFVSNHAY 31

RESULT 10
US-10-878-556A-14
; Sequence 14, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/alfc_human
; DATABASE ENTRY DATE: 1989-03-01
US-10-878-556A-14

Query Match 68.0%; Score 68; DB 5; Length 363;
Best Local Similarity 63.2%; Pred. No. 0.023;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SGQAGAAASESLFISHAY 20
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Db 345 SGEDGGAAAQSLYIANHAY 363

RESULT 11
US-10-170-385-259
; Sequence 259, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100

; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-259

Query Match 68.0%; Score 68; DB 4; Length 364;
Best Local Similarity 63.2%; Pred. No. 0.023;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SGQAGAAASESLFISNHAY 20
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Db 346 SGEDGGAAAQSLYIANHAY 364

RESULT 12
US-10-408-765A-98
; Sequence 98, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-98

Query Match 68.0%; Score 68; DB 4; Length 364;
Best Local Similarity 63.2%; Pred. No. 0.023;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SGQAGAAASESLFISNHAY 20
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Db 346 SGEDGGAAAQSLYIANHAY 364

RESULT 13
US-10-369-493-5923
; Sequence 5923, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5923

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; LENGTH: 365
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5923

Query Match      61.0%; Score 61; DB 4; Length 365;
Best Local Similarity 68.8%; Pred. No. 0.31;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      5 AGAAASESLFISNHAY 20
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Db      350 ADAASQSLFVANHSY 365

RESULT 14
US-10-108-605-255
; Sequence 255, Application US/10108605
; Publication No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
; FILE REFERENCE: 31133B
; CURRENT APPLICATION NUMBER: US/10/108,605
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 09/761,142
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/176,418
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 255
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-108-605-255

Query Match      55.5%; Score 55.5; DB 4; Length 361;
Best Local Similarity 63.2%; Pred. No. 2.4;
Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy      2 SGQAGAAASESLFISNHAY 20
        :| || | | ||||:|||||
Db      344 AGSAG-AGSGSLFVANHAY 361

RESULT 15
US-11-097-143-27699
; Sequence 27699, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24

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; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27699
; LENGTH: 361
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-27699

Query Match 55.5%; Score 55.5; DB 6; Length 361;
Best Local Similarity 63.2%; Pred. No. 2.4;
Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
Qy 2 SGQAGAAASESLFISNHAY 20
:| || | | |||:|||
Db 344 AGSAG-AGSGSLFVANHAY 361

Search completed: July 20, 2006, 09:43:16
Job time : 7.49446 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243 and Search Result us-10-717-243- 57.rapbn.

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:40:39 ; Search time 1.18081 Seconds
(without alignments)
976.754 Million cell updates/sec

Title: US-10-717-243-57
Perfect score: 100
Sequence: 1 PSGQAGAASESFLFISNHAY 20

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Gapop 10.0 , Gapext 0.5

Searched: 208217 seqs, 57668156 residues

Total number of hits satisfying chosen parameters: 208217

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	ID
1	50.5	50.5	836	6	US-10-509-131-35	Sequence 35, App
2	50.5	50.5	836	7	US-11-293-697-3700	Sequence 3700, Ap
3	44.5	44.5	358	6	US-10-449-902-28573	Sequence 28573, A
4	44.5	44.5	358	6	US-10-449-902-28595	Sequence 28595, A
5	44.5	44.5	358	6	US-10-449-902-31655	Sequence 31655, A
6	44.5	44.5	358	6	US-10-449-902-42837	Sequence 42837, A
7	44.5	44.5	358	6	US-10-449-902-53273	Sequence 53273, A
8	43	43.0	443	7	US-11-283-329-128	Sequence 128, App
9	43	43.0	520	6	US-10-449-902-51930	Sequence 51930, A

10	43	43.0	626	7	US-11-283-329-124	Sequence 124, App
11	43	43.0	626	7	US-11-283-329-126	Sequence 126, App
12	43	43.0	637	7	US-11-283-329-130	Sequence 130, App
13	43	43.0	845	7	US-11-056-355B-75212	Sequence 75212, A
14	43	43.0	854	7	US-11-056-355B-45071	Sequence 45071, A
15	43	43.0	854	7	US-11-056-355B-47878	Sequence 47878, A
16	43	43.0	854	7	US-11-056-355B-75211	Sequence 75211, A
17	43	43.0	864	7	US-11-056-355B-45070	Sequence 45070, A
18	43	43.0	864	7	US-11-056-355B-47877	Sequence 47877, A
19	43	43.0	864	7	US-11-056-355B-75210	Sequence 75210, A
20	43	43.0	886	7	US-11-056-355B-45069	Sequence 45069, A
21	43	43.0	886	7	US-11-056-355B-47876	Sequence 47876, A
22	42	42.0	159	7	US-11-056-355B-51219	Sequence 51219, A
23	42	42.0	187	7	US-11-056-355B-51218	Sequence 51218, A
24	42	42.0	271	6	US-10-449-902-33243	Sequence 33243, A
25	42	42.0	307	6	US-10-449-902-44340	Sequence 44340, A
26	42	42.0	674	6	US-10-449-902-43418	Sequence 43418, A
27	41	41.0	1010	7	US-11-056-355B-86864	Sequence 86864, A
28	41	41.0	1035	7	US-11-056-355B-86863	Sequence 86863, A
29	41	41.0	1045	7	US-11-056-355B-73120	Sequence 73120, A
30	40	40.0	128	6	US-10-953-349-3099	Sequence 3099, Ap
31	40	40.0	128	7	US-11-056-355B-28419	Sequence 28419, A
32	40	40.0	128	7	US-11-056-355B-32009	Sequence 32009, A
33	40	40.0	128	7	US-11-056-355B-104705	Sequence 104705,
34	40	40.0	128	7	US-11-056-355B-115944	Sequence 115944,
35	40	40.0	148	6	US-10-953-349-3098	Sequence 3098, Ap
36	40	40.0	148	7	US-11-056-355B-28418	Sequence 28418, A
37	40	40.0	148	7	US-11-056-355B-32008	Sequence 32008, A
38	40	40.0	148	7	US-11-056-355B-104704	Sequence 104704,
39	40	40.0	148	7	US-11-056-355B-115943	Sequence 115943,
40	40	40.0	221	6	US-10-449-902-46304	Sequence 46304, A
41	40	40.0	279	6	US-10-449-902-37961	Sequence 37961, A
42	40	40.0	284	6	US-10-449-902-41709	Sequence 41709, A
43	40	40.0	291	6	US-10-539-868-22	Sequence 22, Appl
44	40	40.0	305	7	US-11-293-697-3972	Sequence 3972, Ap
45	40	40.0	391	7	US-11-056-355B-67785	Sequence 67785, A

ALIGNMENTS

RESULT 1

US-10-509-131-35

; Sequence 35, Application US/10509131
; Publication No. US20060089493A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Inc.
; APPLICANT: McLachlan, Karen
; APPLICANT: Gately, Dennis
; TITLE OF INVENTION: NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CARCINOMAS
; FILE REFERENCE: 037003-0302886
; CURRENT APPLICATION NUMBER: US/10/509,131
; CURRENT FILING DATE: 2004-09-28
; PRIOR APPLICATION NUMBER: US 60/367,727
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/381,328
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/386,747
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/427,564
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-509-131-35

Query Match 50.5%; Score 50.5; DB 6; Length 836;
Best Local Similarity 52.4%; Pred. No. 3.4;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
Qy 1 PSG-QAGAAASESLFISNHAY 20
I:| 1||| | :||: | |

Db 620 PAGPSAGAAGSSTLFLGPHLY 640

RESULT 2
US-11-293-697-3700
; Sequence 3700, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3700
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3700

Query Match 50.5%; Score 50.5; DB 7; Length 836;
Best Local Similarity 52.4%; Pred. No. 3.4;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 1 PSG-QAGAAASESLFISNHAY 20
|:| |||| | :||: ||
Db 620 PAGPSAGAAGSSTLFLGPHLY 640

RESULT 3
US-10-449-902-28573
; Sequence 28573, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28573
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-28573

Query Match 44.5%; Score 44.5; DB 6; Length 358;
Best Local Similarity 52.6%; Pred. No. 13;
Matches 10; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 3 GQAG-AAASESLFISNHAY 20
| | | | ||||: : |
Db 340 GAAGDAATSESLYVKGYTY 358

RESULT 4
US-10-449-902-28595
; Sequence 28595, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28595
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-28595

Query Match 44.5%; Score 44.5; DB 6; Length 358;
Best Local Similarity 52.6%; Pred. No. 13;
Matches 10; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 3 GQAG-AAASESLFISNHAY 20
| || || ||||:: : |
Db 340 GAAGDAATSESLYVKGYTY 358

RESULT 5
US-10-449-902-31655
; Sequence 31655, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31655
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31655

Query Match 44.5%; Score 44.5; DB 6; Length 358;
Best Local Similarity 52.6%; Pred. No. 13;
Matches 10; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 3 GQAG-AAASESLFISNHAY 20
| || || ||||:: : |
Db 340 GAAGDAATSESLYVKGYTY 358

RESULT 6
US-10-449-902-42837
; Sequence 42837, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42837
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-42837

Query Match 44.5%; Score 44.5; DB 6; Length 358;
Best Local Similarity 52.6%; Pred. No. 13;
Matches 10; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 3 GQAG-AAASESLFISNHAY 20
| | | || ||||:: : |
Db 340 GAAGDAATSESLYVKGYTY 358

RESULT 7
US-10-449-902-53273

; Sequence 53273, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53273
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53273

Query Match 44.5%; Score 44.5; DB 6; Length 358;
Best Local Similarity 52.6%; Pred. No. 13;
Matches 10; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 3 GQAG-AAASESLFISNHAY 20
| | | || ||||:: : |
Db 340 GAAGDAATSESLYVKGYTY 358

RESULT 8
US-11-283-329-128

; Sequence 128, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-283-329-128

Query Match 43.0%; Score 43; DB 7; Length 443;
Best Local Similarity 40.0%; Pred. No. 29;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20

Db 224 PLGAAAAGSQAALESHPY 243

RESULT 9

US-10-449-902-51930
; Sequence 51930, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51930
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51930

Query Match 43.0%; Score 43; DB 6; Length 520;
Best Local Similarity 38.2%; Pred. No. 34;
Matches 13; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 PSGQAGAAA-----SESLFISNHAY 20
||| ||| | | | : | : ||
Db 378 PSGQAGATAPLVSPKLEIGKAKGSSSNVLSDPAY 411

RESULT 10

US-11-283-329-124
; Sequence 124, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-283-329-124

Query Match 43.0%; Score 43; DB 7; Length 626;
Best Local Similarity 40.0%; Pred. No. 42;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20
| | | | | | | : | : |
Db 224 PLGAAAAGSQAALESHPY 243

RESULT 11

US-11-283-329-126
; Sequence 126, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS

; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-283-329-126

Query Match 43.0%; Score 43; DB 7; Length 626;
Best Local Similarity 40.0%; Pred. No. 42;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
| | | | | |:: : : | |
Db 224 PLGAAAAGSQAALESHPY 243

RESULT 12
US-11-283-329-130
; Sequence 130, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-283-329-130

Query Match 43.0%; Score 43; DB 7; Length 637;
Best Local Similarity 40.0%; Pred. No. 43;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
| | | | | |:: : : | |
Db 235 PLGAAAAGSQAALESHPY 254

RESULT 13
US-11-056-355B-75212
; Sequence 75212, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 75212
; LENGTH: 845
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(845)
; OTHER INFORMATION: Ceres Seq. ID no. 6431512
US-11-056-355B-75212

Query Match 43.0%; Score 43; DB 7; Length 845;
Best Local Similarity 30.6%; Pred. No. 59;
Matches 11; Conservative 3; Mismatches 6; Indels 16; Gaps 1;

Qy 1 PSGQAGAAA-----SESLFISNHAY 20
||: || | : || || ||
Db 108 PDGEGGATAIHFIGNSWIYPNHRYSRDRVFFSNKAY 143

RESULT 14
US-11-056-355B-45071
; Sequence 45071, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 45071
; LENGTH: 854
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(854)
; OTHER INFORMATION: Ceres Seq. ID no. 12600173
US-11-056-355B-45071

Query Match 43.0%; Score 43; DB 7; Length 854;
Best Local Similarity 30.6%; Pred. No. 59;
Matches 11; Conservative 3; Mismatches 6; Indels 16; Gaps 1;

Qy 1 PSGQAGAAA-----SESLFISNHAY 20
||: || | : || || ||
Db 117 PDGEGGATAIHFIGNSWIYPNHRYSRDRVFFSNKAY 152

RESULT 15
US-11-056-355B-47878
; Sequence 47878, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 47878
; LENGTH: 854
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(854)
; OTHER INFORMATION: Ceres Seq. ID no. 12600173
US-11-056-355B-47878

Query Match 43.0%; Score 43; DB 7; Length 854;
Best Local Similarity 30.6%; Pred. No. 59;
Matches 11; Conservative 3; Mismatches 6; Indels 16; Gaps 1;

Qy 1 PSGQAGAAA-----SESLFISNHAY 20
||: || | : || || ||
Db 117 PDGEGGATAIHFIGNSWIYPNHRYSRDRVFFSNKAY 152

Search completed: July 20, 2006, 09:41:18
Job time : 1.18081 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10717243-57.rpr

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This page gives you Search Results detail for the Application 10717243 and Search Result us-10-71 start

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:36:32 ; Search time 1.51292 Seconds
(without alignments)
1271.939 Million cell updates/sec

Title: US-10-717-243-57
Perfect score: 100
Sequence: 1 PSGQAGAAASESLFISNHAY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	100	100.0	363	1	ADRBA	fructose-bisphosph
2	99	99.0	364	1	ADHUA	fructose-bisphosph
3	97	97.0	364	1	ADMSA	fructose-bisphosph
4	97	97.0	364	1	ADRTA	fructose-bisphosph
5	95	95.0	42	2	I51291	aldolase C - chick
6	77	77.0	364	2	JC4189	fructose-bisphosph
7	69.5	69.5	363	2	JC4188	fructose-bisphosph
8	68	68.0	364	1	ADHUC	fructose-bisphosph
9	61	61.0	365	2	T24514	hypothetical prote
10	60.5	60.5	363	2	I53145	zebrin II - mouse
11	59.5	59.5	363	1	ADRTC	fructose-bisphosph
12	58	58.0	137	2	I51292	aldolase A - chick
13	57	57.0	364	2	S45346	fructose-bisphosph
14	55.5	55.5	361	1	ADEF	fructose-bisphosph
15	55.5	55.5	361	2	C42263	fructose 1,6-bisph
16	52	52.0	366	2	T15951	hypothetical prote
17	50	50.0	364	1	ADRTB	fructose-bisphosph
18	48	48.0	179	2	AF0981	probable exported

19	48	48.0	1772	2	A45532	major merozoite su
20	47	47.0	364	2	S48810	fructose-bisphosph
21	46	46.0	170	2	D95178	conserved domain p
22	46	46.0	170	2	C98045	hypothetical prote
23	46	46.0	293	2	AE1950	cytosine-specific
24	46	46.0	364	1	ADHUB	fructose-bisphosph
25	46	46.0	644	2	T46277	hypothetical prote
26	45	45.0	357	1	ADSPAC	fructose-bisphosph
27	45	45.0	357	2	T12416	fructose-bisphosph
28	45	45.0	364	1	ADCHB	fructose-bisphosph
29	44	44.0	627	2	T02846	dynein light chain
30	44	44.0	1005	2	S73711	probable lipoprote
31	44	44.0	1054	2	T43226	translation initia
32	43	43.0	310	2	B97777	thioredoxin-disulf
33	42	42.0	259	2	T13260	hypothetical prote
34	42	42.0	259	2	D86685	prophage pil prote
35	42	42.0	259	2	C86797	prophage pi3 prote
36	42	42.0	259	2	C86757	prophage pi2 prote
37	42	42.0	307	2	G70665	hypothetical prote
38	42	42.0	310	2	D71703	thioredoxin reduct
39	42	42.0	359	2	S58167	fructose-bisphosph
40	42	42.0	430	2	S66671	neuron-derived rec
41	42	42.0	489	2	F82085	glutamate synthase
42	42	42.0	625	2	S71930	neuron-derived rec
43	42	42.0	628	2	JC2493	neuron derived orp
44	41	41.0	209	2	D64212	D-ribulose-5-phosp
45	41	41.0	242	2	A82512	hypothetical prote

ALIGNMENTS

RESULT 1

ADRBA

fructose-bisphosphate aldolase (EC 4.1.2.13) A - rabbit
 N;Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 24-Apr-1984 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
 C;Accession: A92444; A90059; A90305; A90060; I46474; I46475; A01103
 R;Tolan, D.R.; Amsden, A.B.; Putney, S.D.; Urdea, M.S.; Penhoet, E.E.
J. Biol. Chem. 259, 1127-1131, 1984
 A;Title: The complete nucleotide sequence for rabbit muscle aldolase A messenger RNA.
 A;Reference number: A92444; MUID:84111505; PMID:6546378
 A;Accession: A92444
 A;Molecule type: mRNA
 A;Residues: 1-363
 A;Cross-references: UNIPROT:P00883; UNIPARC:UPI0000125800; GB:K02300; NID:g164751; PIDN:AAA31156.1; PID:g16
 A;Note: initiator Met not shown
 R;Lai, C.Y.; Nakai, N.; Chang, D.
Science 183, 1204-1206, 1974
 A;Title: Amino acid sequence of rabbit muscle aldolase and the structure of the active center.
 A;Reference number: A94244; MUID:74094688; PMID:4812352
 A;Contents: annotation
 A;Note: the sequence reported in this paper has been revised in references A90305 and A90060
 R;Nakai, N.; Chang, D.; Lai, C.Y.
Arch. Biochem. Biophys. 166, 347-357, 1975
 A;Title: Studies on the structure of rabbit muscle aldolase. Ordering of the tryptic peptides; sequence of
 A;Reference number: A90059; MUID:75145171; PMID:1122141
 A;Accession: A90059
 A;Molecule type: protein
 A;Residues: 1-33, 'Q', 35-164
 A;Cross-references: UNIPARC:UPI0000172F31
 R;Benfield, P.A.; Forcina, B.G.; Gibbons, I.; Perham, R.N.
Biochem. J. 183, 429-444, 1979
 A;Title: Extended amino acid sequences around the active-site lysine residue of class-I fructose 1,6-bispho
 A;Reference number: A90305; MUID:80109133; PMID:534504
 A;Accession: A90305
 A;Molecule type: protein
 A;Residues: 173-200
 A;Cross-references: UNIPARC:UPI0000172F32
 R;Lai, C.Y.
Arch. Biochem. Biophys. 166, 358-368, 1975
 A;Title: Studies on the structure of rabbit muscle aldolase. Determination of the primary structure of the
 A;Reference number: A90060; MUID:75145172; PMID:1122142
 A;Accession: A90060
 A;Molecule type: protein

A;Residues: 251-272,'S',274,'E',276-277,'G',279-292,'W',294,'K',296-363
A;Cross-references: UNIPARC:UPI0000172F33
R;Hartman, F.C.; Brown, J.P.
J. Biol. Chem. 251, 3057-3062, 1976
A;Title: Affinity labeling of a previously undetected essential lysyl residue in class I fructose bisphosphatase
A;Reference number: A92191; MUID:76190154; PMID:5453
A;Contents: annotation; active site
R;Putney, S.D.; Herlihy, W.C.; Schimmel, P.
Nature 302, 718-721, 1983
A;Title: A new troponin T and cDNA clones for 13 different muscle proteins, found by shotgun sequencing.
A;Reference number: I46471; MUID:83167564; PMID:6687628
A;Accession: I46474
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 37-55
A;Cross-references: UNIPARC:UPI000016C530; EMBL:V00876; NID:g1444; PIDN:CAA24245.1; PID:g929753
A;Accession: I46475
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 349-352,'R',354-363
A;Cross-references: UNIPARC:UPI000016C531; EMBL:V00877; NID:g1446; PIDN:CAA24246.1; PID:g833792
C;Comment: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, aldolase A in muscle
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; pentose phosphate pathway
F;2-363/Product: fructose-bisphosphate aldolase A #status predicted
F;146,229,363/Active site: Lys, Lys, Tyr #status predicted

```

Query Match           100.0%; Score 100; DB 1; Length 363;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PSGQAGAAASESLFISNHAY 20
       ||||||| | | | | | | | |
Db      344 PSGOAGAAASESLFISNHAY 363

```

RESULT 2

ADHUA
fructose-bisphosphate aldolase (EC 4.1.2.13) A [validated] - human
N;Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S14084; A27186; S01014; S00290; S02338; A05177; S03874; S23919; I39429; I39435
R;Mukai, T.; Arai, Y.; Yatsuki, H.; Joh, K.; Hori, K.
Eur. J. Biochem. 195, 781-787, 1991
A;Title: An additional promoter functions in the human aldolase A gene, but not in rat.
A;Reference number: S14084; MUID:91153319; PMID:1999195
A;Accession: S14084
A;Molecule type: DNA
A;Residues: 1-364
A;Cross-references: UNIPROT:P04075; UNIPARC:UPI0000000C5D
R;Izzo, P.; Costanzo, P.; Lupo, A.; Rippa, E.; Borghese, A.M.; Paolella, G.; Salvatore, F.
Eur. J. Biochem. 164, 9-13, 1987
A;Title: A new human species of aldolase A mRNA from fibroblasts.
A;Reference number: A27186; MUID:87161904; PMID:3030757
A;Accession: A27186
A;Molecule type: mRNA
A;Residues: 1-364
A;Cross-references: UNIPARC:UPI0000000C5D; GB:X05236; NID:g28596; PIDN:CAA28861.1; PID:g28597
A;Experimental source: fibroblast
R;Izzo, P.; Costanzo, P.; Lupo, A.; Rippa, E.; Paolella, G.; Salvatore, F.
Eur. J. Biochem. 174, 569-578, 1988
A;Title: Human aldolase A gene. Structural organization and tissue-specific expression by multiple promoter
A;Reference number: S01014; MUID:88271327; PMID:3391172
A;Accession: S01014
A;Molecule type: DNA
A;Residues: 1-72,'G',74-195,'A',197-229,'N',231-279,'S',281-364
A;Cross-references: UNIPARC:UPI000016A52D; GB:X12447; NID:g28613; PIDN:CAA30979.1; PID:g28614
R;Freemont, P.S.; Dunbar, B.; Fothergill-Gilmore, L.A.
Biochem. J. 249, 779-788, 1988
A;Title: The complete amino acid sequence of human skeletal-muscle fructose-bisphosphate aldolase.
A;Reference number: S00290; MUID:88183272; PMID:3355497
A;Accession: S00290
A;Molecule type: protein
A;Residues: 2-358,'I',360-364
A;Cross-references: UNIPARC:UPI0000172F2C

R;Maire, P.; Gautron, S.; Hakim, V.; Gregori, C.; Mennecier, F.; Kahn, A.
J. Mol. Biol. 197, 425-438, 1987
A;Title: Characterization of three optional promoters in the 5' region of the human aldolase A gene.
A;Reference number: S02338; MUID:88155643; PMID:3441006
A;Accession: S02338
A;Molecule type: DNA
A;Residues: 1-108
A;Cross-references: UNIPARC:UPI000016A521; EMBL:X06352; NID:g28594; PIDN:CAA29654.1; PID:g28595
R;Freemont, P.S.; Dunbar, B.; Fothergill, L.A.
Arch. Biochem. Biophys. 228, 342-352, 1984
A;Title: Human skeletal-muscle aldolase: N-terminal sequence analysis of CNBr- and o-iodosobenzoic acid-cle
A;Reference number: A05177; MUID:84126818; PMID:6696436
A;Accession: A05177
A;Molecule type: protein
A;Residues: 2-63;148-358
A;Cross-references: UNIPARC:UPI0000172F2D; UNIPARC:UPI0000172F2E
R;Sakakibara, M.; Takahashi, I.; Takasaki, Y.; Mukai, T.; Hori, K.
Biochim. Biophys. Acta 1007, 334-342, 1989
A;Title: Construction and expression of human aldolase A and B expression plasmids in Escherichia coli host
A;Reference number: S03874; MUID:89194215; PMID:2649152
A;Accession: S03874
A;Molecule type: mRNA
A;Residues: 1-33;357-364
A;Cross-references: UNIPARC:UPI0000172F2F; UNIPARC:UPI0000172F30
R;Lee, K.N.; Maxwell, M.D.; Patterson Jr., M.K.; Birckbichler, P.J.; Conway, E.
Biochim. Biophys. Acta 1136, 12-16, 1992
A;Title: Identification of transglutaminase substrates in HT29 colon cancer cells: use of 5-(biotinamido) p
A;Reference number: S23919; MUID:92353128; PMID:1353685
A;Accession: S23919
A;Molecule type: protein
A;Residues: 2-16
A;Cross-references: UNIPARC:UPI0000071F95
R;Gamblin, S.J.; Davies, G.J.; Grimes, J.M.; Jackson, R.M.; Littlechild, J.A.; Watson, H.C.
J. Mol. Biol. 219, 573-576, 1991
A;Title: Activity and Specificity of Human Aldolases.
A;Reference number: A43787; MUID:91278081; PMID:2056525
A;Contents: annotation; active site
R;Sakakibara, M.; Mukai, T.; Hori, K.
Biochem. Biophys. Res. Commun. 131, 413-420, 1985
A;Title: Nucleotide sequence of a cDNA clone for human aldolase: a messenger RNA in the liver.
A;Reference number: I39429; MUID:85306986; PMID:3840020
A;Accession: I39429
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-364
A;Cross-references: UNIPARC:UPI0000000C5D; GB:M11560; NID:g178350; PIDN:AAA51690.1; PID:g178351
R;Tolan, D.R.; Niclas, J.; Bruce, B.D.; Lebo, R.V.
Am. J. Hum. Genet. 41, 907-924, 1987
A;Title: Evolutionary implications of the human aldolase-A, -B, -C, and -pseudogene chromosome locations.
A;Reference number: I39435; MUID:88046782; PMID:3674018
A;Accession: I39435
A;Molecule type: mRNA
A;Residues: 139-364
A;Cross-references: UNIPARC:UPI000016A52E; GB:M21190; NID:g178403; PIDN:AAA51697.1; PID:g178404
C;Comment: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, aldolase A in muscle
C;Genetics:
A;Gene: GDB:ALDOA
A;Cross-references: GDB:118993; OMIM:103850
A;Map position: 16q22.2-16q22.2
A;Introns: 38/1
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; pentose phosphate pat
F;2-364/Product: fructose-bisphosphate aldolase A #status experimental
F;147,230,364/Active site: Lys, Lys, Tyr #status experimental

Query Match 99.0%; Score 99; DB 1; Length 364;
Best Local Similarity 95.0%; Pred. No. 2.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||:|||||:|||||
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 3
ADMSA

fructose-bisphosphate aldolase (EC 4.1.2.13) A - mouse
 N;Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C;Accession: S06323; B25388; A37062
 R;Mestek, A.; Stauffer, J.; Tolan, D.R.; Ciejek-Baez, E.
Nucleic Acids Res. 15, 10595, 1987
 A;Title: Sequence of a mouse brain aldolase A cDNA.
 A;Reference number: S06323; MUID:88096598; PMID:3697100
 A;Accession: S06323
 A;Molecule type: mRNA
 A;Residues: 1-364
 A;Cross-references: UNIPROT:P05064; UNIPARC:UPI000000B2CC; GB:Y00516; NID:g49914; PIDN:CAA68571.1; PID:g499
 A;Experimental source: brain
 R;Paolella, G.; Buono, P.; Mancini, F.P.; Izzo, P.; Salvatore, F.
Eur. J. Biochem. 156, 229-235, 1986
 A;Title: Structure and expression of mouse aldolase genes. Brain-specific aldolase C amino acid sequence is
 A;Reference number: A91165; MUID:86192445; PMID:3009179
 A;Accession: B25388
 A;Molecule type: mRNA
 A;Residues: 99-280,'C',282-355
 A;Cross-references: UNIPARC:UPI000016CBFC; GB:X03797; NID:g49916; PIDN:CAA27423.1; PID:g929677
 A;Experimental source: brain
 R;Stauffer, J.K.; Colbert, M.C.; Ciejek-Baez, E.
J. Biol. Chem. 265, 11773-11782, 1990
 A;Title: Nonconservative utilization of aldolase A alternative promoters.
 A;Reference number: A37062; MUID:90307699; PMID:2365699
 A;Accession: A37062
 A;Molecule type: DNA
 A;Residues: 1-266;295-364
 A;Cross-references: UNIPARC:UPI0000172F34; UNIPARC:UPI0000172F35; GB:J05517
 A;Experimental source: strain RIII S/J
 C;Superfamily: fructose-bisphosphate aldolase
 C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; pentose phosphate pat
 F;2-364/Product: fructose-bisphosphate aldolase A #status predicted
 F;147,230,364/Active site: Lys, Lys, Tyr #status predicted

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Query Match          97.0%;  Score 97;  DB 1;  Length 364;
Best Local Similarity  95.0%;  Pred. No. 5.2e-08;
Matches   19;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 PSGQAGAAASESLFISHAY 20
       ||||:||||||||||||||| |
Db      345 PSGQSGAAASESLFISHAY 364
  
```

RESULT 4
ADRTA
 fructose-bisphosphate aldolase (EC 4.1.2.13) A - rat
 N;Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Dec-2004
 C;Accession: A24532; A25383; I53307; I56408
 R;Joh, K.; Mukai, T.; Yatsuki, H.; Hori, K.
Gene 39, 17-24, 1985
 A;Title: Rat aldolase A messenger RNA: the nucleotide sequence and multiple mRNA species with different 5'-
 A;Reference number: A24532; MUID:86083188; PMID:2416636
 A;Accession: A24532
 A;Molecule type: mRNA
 A;Residues: 1-364
 A;Cross-references: UNIPROT:P05065; UNIPROT:Q63038; UNIPARC:UPI0000170873; GB:M14420; NID:g202836; PIDN:AAA
 R;Mukai, T.; Joh, K.; Arai, Y.; Yatsuki, H.; Hori, K.
J. Biol. Chem. 261, 3347-3354, 1986
 A;Title: Tissue-specific expression of rat aldolase A mRNAs: three molecular species differing only in the
 A;Reference number: A25383; MUID:86140113; PMID:3753977
 A;Accession: A25383
 A;Molecule type: mRNA
 A;Residues: 1-144,'F',146-164,'M',166-364
 A;Cross-references: UNIPARC:UPI0000167983; GB:M12919; NID:g202834; PIDN:AAA40714.1; PID:g202835
 R;Tsutsumi, R.; Tsutsumi, K.
Eur. J. Biochem. 142, 161-164, 1984
 A;Title: Two different aldolase A mRNA species in rat tissues.
 A;Reference number: I53307; MUID:84261525; PMID:6086339
 A;Accession: I53307
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA

A;Residues: 324-329, 'Q', 331-356
A;Cross-references: UNIPARC:UPI00000E7075; GB:M28282; NID:g202849; PIDN:AAA40720.1; PID:g202850
R;Joh, K.; Arai, Y.; Mukai, T.; Hori, K.
J. Mol. Biol. 190, 401-410, 1986
A;Title: Expression of three mRNA species from a single rat aldolase A gene, differing in their 5' non-codi
A;Reference number: I56408; MUID:87060996; PMID:3783705
A;Accession: I56408
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-108
A;Cross-references: UNIPARC:UPI0000172F36; EMBL:X04261; NID:g55639; PIDN:CAA27815.1; PID:g1619605
C;Genetics:
A;Introns: 38/1
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; pentose phosphate pat
F;2-364/Product: fructose-bisphosphate aldolase A #status predicted
F;147,230,364/Active site: Lys, Lys, Tyr #status predicted

Query Match 97.0%; Score 97; DB 1; Length 364;
Best Local Similarity 95.0%; Pred. No. 5.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||||||||||||
Db 345 PSGQSGAAASESLFISHAY 364

RESULT 5
I51291
aldolase C - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C;Accession: I51291
R;Meighan-Mantha, R.L.; Tolan, D.R.
J. Cell. Biochem. 57, 423-431, 1995
A;Title: Noncoordinate changes in the steady-state mRNA expressed from aldolase A and aldolase C genes duri
A;Reference number: I51291; MUID:95286677; PMID:7768978
A;Accession: I51291
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-42
A;Cross-references: UNIPROT:Q92007; UNIPARC:UPI00000FDF44; GB:S78288; NID:g999389; PIDN:AAB34479.1; PID:g99
C;Superfamily: fructose-bisphosphate aldolase

Query Match 95.0%; Score 95; DB 2; Length 42;
Best Local Similarity 95.0%; Pred. No. 1e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
||| |||||||||||||||||
Db 23 PSGHAGAAASESLFISHAY 42

RESULT 6
JC4189
fructose-bisphosphate aldolase (EC 4.1.2.13), non-muscle-type - Pacific lamprey
N;Alternate names: non-muscle-type aldolase
C;Species: Lampetra tridentata, Entosphenus tridentatus (Pacific lamprey)
C;Date: 27-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C;Accession: JC4189
R;Zhang, R.; Yatsuki, H.; Kusakabe, T.; Iwabe, N.; Miyata, T.; Imai, T.; Yoshida, M.; Hori, K.
J. Biochem. 117, 545-553, 1995
A;Title: Structures of cDNAs encoding the muscle-type and non-muscle-type isozymes of lamprey fructose bisp
A;Reference number: JC4188; MUID:95355304; PMID:7629020
A;Accession: JC4189
A;Molecule type: mRNA
A;Residues: 1-364
A;Cross-references: UNIPARC:UPI00001257F9; DDBJ:D38619; NID:g1619826; PIDN:BAA07607.1; PID:g974730
C;Comment: This is a glycolytic enzyme that catalyzes the reversible cleavage of fructose-1,6-bisphosphate
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; muscle
F;230/Active site: Lys #status predicted

Query Match 77.0%; Score 77; DB 2; Length 364;
Best Local Similarity 70.0%; Pred. No. 9.4e-05;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|:| :|:|||||||:|| |
Db 345 PAGSSGSAASESLFIANHNY 364

RESULT 7

JC4188

fructose-bisphosphate aldolase (EC 4.1.2.13), muscle-type - Pacific lamprey
N;Alternate names: muscle-type aldolase
C;Species: Lampetra tridentata, Entosphenus tridentatus (Pacific lamprey)
C;Date: 27-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C;Accession: JC4188
R;Zhang, R.; Yatsuki, H.; Kusakabe, T.; Iwabe, N.; Miyata, T.; Imai, T.; Yoshida, M.; Hori, K.
J. Biochem. 117, 545-553, 1995
A;Title: Structures of cDNAs encoding the muscle-type and non-muscle-type isozymes of lamprey fructose bisp
A;Reference number: JC4188; MUID:95355304; PMID:7629020
A;Accession: JC4188
A;Molecule type: mRNA
A;Residues: 1-363
A;Cross-references: UNIPARC:UPI00001257EF; DDBJ:D38620; NID:g1619827; PIDN:BAA07608.1; PID:g974732
C;Comment: This is a glycolytic enzyme that catalyzes the reversible cleavage of fructose-1,6-bisphosphate
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; muscle
F;230/Active site: Lys #status predicted

Query Match 69.5%; Score 69.5; DB 2; Length 363;
Best Local Similarity 70.0%; Pred. No. 0.0016;
Matches 14; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 1 PSGQAGAAASESLFISHAY 20
|:| :|:|||||||:|| |
Db 345 PTG-TGAAAGESLFWANHAY 363

RESULT 8

ADHUC

fructose-bisphosphate aldolase (EC 4.1.2.13) C - human
N;Alternate names: aldolase C; fructose-1,6-bisphosphate triosephosphate-lyase C
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: A25861; S00863; S13192
R;Rottmann, W.H.; Deselms, K.R.; Niclas, J.; Camerato, T.; Holman, P.S.; Green, C.J.; Tolan, D.R.
Biochimie 69, 137-145, 1987
A;Title: The complete amino acid sequence of the human aldolase C isozyme derived from genomic clones.
A;Reference number: A25861; MUID:87185595; PMID:3105602
A;Accession: A25861
A;Molecule type: DNA
A;Residues: 1-364
A;Cross-references: UNIPROT:P09972; UNIPARC:UPI0000000C53; GB:X05196; NID:g28598; PIDN:CAA28825.1; PID:g285
R;Buono, P.; Paoletta, G.; Mancini, F.P.; Izzo, P.; Salvatore, F.
Nucleic Acids Res. 16, 4733, 1988
A;Title: The complete nucleotide sequence of the gene coding for the human aldolase C.
A;Reference number: S00863; MUID:88247784; PMID:3267224
A;Accession: S00863
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-310, 'V', 312-364
A;Cross-references: UNIPARC:UPI000016A523; GB:X07292; NID:g28600; PIDN:CAA30270.1; PID:g312137
R;Buono, P.; Mancini, F.P.; Izzo, P.; Salvatore, F.
Eur. J. Biochem. 192, 805-811, 1990
A;Title: Characterization of the transcription-initiation site and of the promoter region within the 5' fla
A;Reference number: S13192; MUID:91006178; PMID:2209624
A;Accession: S13192
A;Molecule type: DNA
A;Residues: 1-310, 'V', 312-364
A;Cross-references: UNIPARC:UPI000016A523; GB:X07292; GB:M84921; NID:g28600; PIDN:CAA30270.1; PID:g312137
C;Genetics:
A;Gene: GDB:ALDOC
A;Cross-references: GDB:119670; OMIM:103870
A;Map position: 17pter-17qter
A;Introns: 38/1; 108/3; 127/1; 180/3; 208/3; 267/1; 333/3
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; brain; carbon-carbon lyase; gluconeogenesis; glycolysis; pentose phosphate path
F;2-364/Product: fructose-bisphosphate aldolase C #status predicted
F;147, 230, 364/Active site: Lys, Lys, Tyr #status predicted

Query Match 68.0%; Score 68; DB 1; Length 364;
Best Local Similarity 63.2%; Pred. No. 0.0028;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SGQAGAAASESLFISNHAY 20
||: | ||::||:|:||||
Db 346 SGDGGAAAQSLYIANHAY 364

RESULT 9
T24514
hypothetical protein T05D4.1 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24514
R;McMurray, A.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19902
A;Accession: T24514
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-365
A;Cross-references: UNIPROT:P54216; UNIPARC:UPI0000164172; EMBL:Z81115; PIDN:CAB03291.1; GSPDB:GN00021; CES
A;Experimental source: clone T05D4
C;Genetics:
A;Gene: CESP:T05D4.1
A;Map position: 3
A;Introns: 32/1; 190/3
C;Superfamily: fructose-bisphosphate aldolase

Query Match 61.0%; Score 61; DB 2; Length 365;
Best Local Similarity 68.8%; Pred. No. 0.038;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGAAASESLFISNHAY 20
| ||||:|||:||:||:
Db 350 ADAASQSLFVANHSY 365

RESULT 10
I53145
zebrin II - mouse
C;Species: *Mus sp. (mouse)*
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
C;Accession: I53145
R;Ahn, A.H.; Dziennis, S.; Hawkes, R.; Herrup, K.
Development 120, 2081-2090, 1994
A;Title: The cloning of zebrin II reveals its identity with aldolase C.
A;Reference number: I53145; MUID:95009537; PMID:7925012
A;Accession: I53145
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-363
A;Cross-references: UNIPARC:UPI0000E5AF7; GB:S72537; NID:g619372; PIDN:AAB32064.1; PID:g619373
C;Superfamily: fructose-bisphosphate aldolase

Query Match 60.5%; Score 60.5; DB 2; Length 363;
Best Local Similarity 68.4%; Pred. No. 0.046;
Matches 13; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 2 SGQAGAAASESLFISNHAY 20
|| |||| :||:|:||||
Db 346 SGDGGAAA-QSLYIANHAY 363

RESULT 11
ADRTC
fructose-bisphosphate aldolase (EC 4.1.2.13) C - rat
N;Alternate names: aldolase C; fructose-1,6-bisphosphate triosephosphate-lyase C; fructose-bisphosphate ald
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Dec-2004
C;Accession: S00326; A38817; JN0127; I53313
R;Kukita, A.; Mukai, T.; Miyata, T.; Hori, K.
Eur. J. Biochem. 171, 471-478, 1988
A;Title: The structure of brain-specific rat aldolase C mRNA and the evolution of aldolase isozyme genes.
A;Reference number: S00326; MUID:88151941; PMID:2831050

A;Accession: S00326
 A;Molecule type: mRNA
 A;Residues: 1-363
 A;Cross-references: UNIPROT:P09117; UNIPROT:Q63037; UNIPARC:UPI0000172F37; EMBL:X06984; NID:g55634; PIDN:CA
 A;Accession: A38817
 A;Molecule type: protein
 A;Residues: 2-21
 A;Cross-references: UNIPARC:UPI0000172F38
 R;Mukai, T.; Yatsuki, H.; Masuko, S.; Arai, Y.; Joh, K.; Hori, K.
Biochem. Biophys. Res. Commun. 174, 1035-1042, 1991
 A;Title: The structure of the brain-specific rat aldolase C gene and its regional expression.
 A;Reference number: JN0127; MUID:91128359; PMID:1993044
 A;Accession: JN0127
 A;Molecule type: DNA
 A;Residues: 1-336, 'LAA', 340-363
 A;Cross-references: UNIPARC:UPI0000000082; GB:M63656; NID:g202841; PIDN:AAA40717.1; PID:g202842
 R;Skala, H.; Vibert, M.; Lamas, E.; Maire, P.; Schweighoffer, F.; Kahn, A.
Eur. J. Biochem. 163, 513-518, 1987
 A;Title: Molecular cloning and expression of rat aldolase C messenger RNA during development and hepatocarc
 A;Reference number: I53313; MUID:87161851; PMID:3830170
 A;Accession: I53313
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 251-363
 A;Cross-references: UNIPARC:UPI00000E7060; EMBL:X05277; NID:g55632; PIDN:CAA28889.1; PID:g55633
 C;Genetics:
 A;Introns: 38/1; 108/3; 127/1; 180/3; 208/3; 267/1; 333/3
 C;Keywords: aldehyde-lyase; brain; carbon-carbon lyase; gluconeogenesis; glycolysis; pentose phosphate path
 F;2-363/Product: fructose-bisphosphate aldolase C #status experimental
 F;147,230,363/Active site: Lys, Lys, Tyr #status predicted

```

Query Match      59.5%; Score 59.5; DB 1; Length 363;
Best Local Similarity 63.2%; Pred. No. 0.067;
Matches 12; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy      2 SGQAGAAASESLFISNHAY 20
        || |||| :||:::|||||
Db      346 SGDGGAAA-QSLYVANHAY 363
  
```

RESULT 12
 I51292
 aldolase A - chicken (fragment)
 C;Species: Gallus gallus (chicken)
 C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
 C;Accession: I51292
 R;Meighan-Mantha, R.L.; Tolan, D.R.
J. Cell. Biochem. 57, 423-431, 1995
 A;Title: Noncoordinate changes in the steady-state mRNA expressed from aldolase A and aldolase C genes duri
 A;Reference number: I51291; MUID:95286677; PMID:7768978
 A;Accession: I51292
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-137
 A;Cross-references: UNIPROT:P53449; UNIPARC:UPI0000125808; GB:S78291; NID:g999391; PIDN:AAB34480.1; PID:g99
 C;Superfamily: fructose-bisphosphate aldolase

```

Query Match      58.0%; Score 58; DB 2; Length 137;
Best Local Similarity 52.6%; Pred. No. 0.041;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      2 SGQAGAAASESLFISNHAY 20
        || || :||:::|||||
Db      119 SGDDSGAAGQSLYVANHAY 137
  
```

RESULT 13
 S45346
 fructose-bisphosphate aldolase (EC 4.1.2.13) C, brain-type - African clawed frog
 N;Alternate names: aldolase C
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 16-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
 C;Accession: S45346; I51247
 R;Atsushi, Y.; Yamana, K.; Yatsuki, H.; Hori, K.; Ueda, S.; Shiokawa, K.
Biochim. Biophys. Acta 1218, 153-157, 1994
 A;Title: Cloning of a brain-type aldolase cDNA and changes in its mRNA level during oogenesis and early emb

A;Reference number: I51247; MUID:94289472; PMID:8018714
A;Accession: S45346
A;Molecule type: mRNA
A;Residues: 1-364
A;Cross-references: UNIPROT:Q91384; UNIPARC:UPI00000FBC29; GB:S73606; NID:g688323; PIDN:AAB31152.1; PID:g68
A;Experimental source: brain
A;Note: translation of initiator Met is not shown
C;Genetics:
A;Gene: XALD3
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase
F;2-364/Product: fructose-bisphosphate aldolase C #status predicted

Query Match 57.0%; Score 57; DB 2; Length 364;
Best Local Similarity 47.4%; Pred. No. 0.17;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SGQAGAAASESLFISNHAY 20
|| :| :||:::||||
Db 346 SGDAGSAGQSLYVANHAY 364

RESULT 14
ADFF
fructose-bisphosphate aldolase (EC 4.1.2.13) - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 30-Sep-1991 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: B42027; S06439; A28855; S22186
R;Kim, J.; Yim, J.J.; Wang, S.; Dorsett, D.
Mol. Cell. Biol. 12, 773-783, 1992
A;Title: Alternate use of divergent forms of an ancient exon in the fructose-1,6-bisphosphate aldolase gene
A;Reference number: A42027; MUID:92123202; PMID:1732743
A;Accession: B42027
A;Molecule type: DNA
A;Residues: 1-361
A;Cross-references: UNIPROT:P07764; UNIPARC:UPI000016BACB; EMBL:X60064; NID:g7571; PIDN:CAA42667.1; PID:g75
A;Note: sequence extracted from NCBI backbone (NCBIN:76664, NCBIPI:87828)
R;Malek, A.A.; Hy, M.; Honegger, A.; Rose, K.; Brenner-Holzach, O.
Arch. Biochem. Biophys. 266, 10-31, 1988
A;Title: Fructose-1,6-bisphosphate aldolase from *Drosophila melanogaster*: primary structure analysis, secon
A;Reference number: S06439; MUID:89024658; PMID:3140728
A;Accession: S06439
A;Molecule type: protein
A;Residues: 2-110,'K',112-200,'R',202-250,'A',252-361
A;Cross-references: UNIPARC:UPI0000125817
R;Brenner-Holzach, O.; Zumsteg, C.
Arch. Biochem. Biophys. 214, 89-101, 1982
A;Title: Fructose 1,6-bisphosphate aldolase of *Drosophila melanogaster*: comparative sequence analyses aroun
A;Reference number: A28855; MUID:82205133; PMID:6805442
A;Accession: A28855
A;Molecule type: protein
A;Residues: 170-179,'QS',182-200,'R',202-224,'Q',226-250,'A',252-272
A;Cross-references: UNIPARC:UPI0000172F3D
A;Note: peptides were ordered by homology with the rabbit sequence
C;Genetics:
A;Gene: FlyBase:Ald
A;Cross-references: FlyBase:FBgn0000064
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; pentose phosphate pathway
F;2-361/Product: fructose-bisphosphate aldolase #status experimental
F;147,230,361/Active site: Lys, Lys, Tyr #status predicted

Query Match 55.5%; Score 55.5; DB 1; Length 361;
Best Local Similarity 63.2%; Pred. No. 0.3;
Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 2 SGQAGAAASESLFISNHAY 20
:| || | | ||:::||||
Db 344 AGSAG-AGSGSLFVANHAY 361

RESULT 15
C42263
fructose 1,6-bisphosphate aldolase - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: C42263
R;Shaw-Lee, R.; Lissemore, J.L.; Sullivan, D.T.; Tolan, D.R.
J. Biol. Chem. 267, 3959-3967, 1992
A;Title: Alternative splicing of fructose 1,6-bisphosphate aldolase transcripts in *Drosophila melanogaster*
A;Reference number: A42263; MUID:92156139; PMID:1740444
A;Accession: C42263
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-361
A;Cross-references: UNIPROT:P07764; UNIPARC:UPI00001248A2; GB:M98351; GB:M76409; NID:g157395; PIDN:AAA99428
A;Note: sequence extracted from NCBI backbone (NCBIN:82659, NCBIPI:93286)
C;Genetics:
A;Gene: FlyBase:Ald
A;Cross-references: FlyBase:FBgn0000064
C;Superfamily: fructose-bisphosphate aldolase

Query Match 55.5%; Score 55.5; DB 2; Length 361;
Best Local Similarity 63.2%; Pred. No. 0.3;
Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 2 SGQAGAAASESLFISNHAY 20
:| || | | |||:|||
Db 344 AGSAG-AGSGSLFVANHAY 361

Search completed: July 20, 2006, 09:37:21
Job time : 2.51292 secs

SCORE 1.3 BuildDate: 12/06/2

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:36:29 ; Search time 20.5535 Seconds
(without alignments)
900.105 Million cell updates/sec

Title: US-10-717-243-57
Perfect score: 100
Sequence: 1 PSGQAGAAASESLFISNHAY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	100	100.0	363	1	ALDOA_RABIT	P00883 oryctolagus
2	99	99.0	260	2	Q9BWD9_HUMAN	Q9bwd9 homo sapien
3	99	99.0	363	1	ALDOA_HUMAN	P04075 homo sapien
4	99	99.0	364	2	Q6FI10_HUMAN	Q6fi10 homo sapien
5	99	99.0	364	2	Q5NVR5_PONPY	Q5nvr5 pongo pygma
6	97	97.0	363	1	ALDOA_MOUSE	P05064 mus musculu
7	97	97.0	363	1	ALDOA_RAT	P05065 rattus norv
8	97	97.0	364	2	Q5FWB7_MOUSE	Q5fbw7 m aldolase
9	97	97.0	364	2	Q6NY00_MOUSE	Q6ny00 mus musculu
10	95	95.0	42	2	Q92007_CHICK	Q92007 gallus gall
11	94	94.0	276	2	Q4R523_MACFA	Q4r523 macaca fasc
12	94	94.0	704	2	Q8WNT7_MACFA	Q8wnt7 macaca fasc
13	89	89.0	331	2	Q76BG8_AMBME	Q76bg8 ambystoma m
14	88	88.0	364	2	Q9CPQ9_MOUSE	Q9cpq9 m adult mal
15	88	88.0	364	2	Q9CRC1_MOUSE	Q9crc1 m adult mal

16	85	85.0	364	2	Q6GL64_XENTR	Q6gl64 xenopus tro
17	83	83.0	364	2	Q6AY07_RAT	Q6ay07 rattus norv
18	83	83.0	364	2	O12975_XENLA	O12975 xenopus lae
19	82	82.0	331	2	Q76BE7_AMICA	Q76be7 amia calva
20	79	79.0	279	2	Q7SYU5_XENLA	Q7syu5 xenopus lae
21	79	79.0	331	2	Q76BF4_LEPOS	Q76bf4 lepisosteus
22	79	79.0	364	2	Q3KPP7_XENLA	Q3kpp7 xenopus lae
23	79	79.0	364	2	Q5XGT3_XENLA	Q5xgt3 xenopus lae
24	77	77.0	364	1	ALF2_LAMJA	P53446 lampetra ja
25	76	76.0	331	2	Q76BI2_PROAN	Q76bi2 protopterus
26	75	75.0	364	2	Q803Q7_BRARE	Q803q7 brachydanio
27	75	75.0	364	2	Q8JH72_BRARE	Q8jh72 brachydanio
28	74	74.0	331	2	Q76BB1_9CHON	Q76bb1 callorhinch
29	73	73.0	331	2	Q76BC5_9CHON	Q76bc5 cephaloscyll
30	72	72.0	331	2	Q76BD2_POLOR	Q76bd2 polypterus
31	72	72.0	364	2	Q6P043_BRARE	Q6p043 brachydanio
32	71	71.0	331	2	Q76BD9_ACIBE	Q76bd9 acipenser b
33	71	71.0	331	2	Q9U5F9_EPTBU	Q9u5f9 eptatretus
34	70	70.0	331	2	Q76BE0_ACIBE	Q76be0 acipenser b
35	69.5	69.5	363	1	ALF1_LAMJA	P53445 lampetra ja
36	69	69.0	331	2	Q76BB8_9CHON	Q76bb8 potamotrygo
37	69	69.0	364	2	Q72W73_BRARE	Q7zw73 brachydanio
38	68	68.0	363	1	ALDOC_HUMAN	P09972 homo sapien
39	68	68.0	363	1	ALDOC_MACFA	Q9gkw3 macaca fasc
40	68	68.0	363	1	ALDOC_PANTR	Q5rlx4 pan troglod
41	68	68.0	364	2	Q6FH94_HUMAN	Q6fh94 homo sapien
42	68	68.0	364	2	Q4R4S9_MACFA	Q4r4s9 macaca fasc
43	68	68.0	394	2	Q6POL5_HUMAN	Q6p015 homo sapien
44	68	68.0	398	2	Q3SYL3_HUMAN	Q3syl3 homo sapien
45	65	65.0	331	2	Q76BC3_9CHON	Q76bc3 cephaloscyll

ALIGNMENTS

RESULT 1
ALDOA_RABIT

ID ALDOA_RABIT STANDARD; PRT; 363 AA.
AC P00883; Q28671;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-FEB-2006, entry version 61.
DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase).
GN Name=ALDOA;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=74094688; PubMed=4812352;
RA Lai C.-Y., Nakai N., Chang D.;
RT "Amino acid sequence of rabbit muscle aldolase and the structure of
the active center.";
RL Science 183:1204-1206(1974).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=84111505; PubMed=6546378;
RA Tolan D.R., Amsden A.B., Putney S.D., Urdea M.S., Penhoet E.E.;
RT "The complete nucleotide sequence for rabbit muscle aldolase A
messenger RNA.";
RL J. Biol. Chem. 259:1127-1131(1984).
RN [3]
RP PROTEIN SEQUENCE OF 1-164.
RX MEDLINE=75145171; PubMed=11222141;
RA Nakai N., Chang D., Lai C.-Y.;
RT "Studies on the structure of rabbit muscle aldolase. Ordering of the
tryptic peptides; sequence of 164 amino acid residues in the NH2-
terminal BrCN peptide.";
RL Arch. Biochem. Biophys. 166:347-357(1975).
RN [4]
RP PROTEIN SEQUENCE OF 173-200, AND SEQUENCE REVISION.
RX MEDLINE=80109133; PubMed=534504;
RA Benfield P.A., Forcina B.G., Gibbons I., Perham R.N.;
RT "Extended amino acid sequences around the active-site lysine residue

RT of class-I fructose 1,6-bisphosphate aldolases from rabbit muscle,
RT sturgeon muscle, trout muscle and ox liver.";
RL Biochem. J. 183:429-444(1979).
RN [5]
RP PROTEIN SEQUENCE OF 251-363, AND SEQUENCE REVISION.
RX MEDLINE=75145172; PubMed=1122142;
RA Lai C.-Y.;
RT "Studies on the structure of rabbit muscle aldolase. Determination of
RT the primary structure of the COOH-terminal BrCN peptide; the complete
RT sequence of the subunit polypeptide chain.";
RL Arch. Biochem. Biophys. 166:358-368(1975).
RN [6]
RP NUCLEOTIDE SEQUENCE [mRNA] OF 37-55 AND 349-363.
RX MEDLINE=83167564; PubMed=6687628;
RA Putney S.D., Herlihy W.C., Schimmel P.R.;
RT "A new troponin T and cDNA clones for 13 different muscle proteins,
RT found by shotgun sequencing.";
RL Nature 302:718-721(1983).
RN [7]
RP ACTIVE SITE.
RX MEDLINE=74163196; PubMed=4857186;
RA Hartman F.C., Welch M.H.;
RT "Identification of the histidyl residue of rabbit muscle aldolase
RT alkylated by N-bromoacetyl-ethanolamine phosphate.";
RL Biochem. Biophys. Res. Commun. 57:85-92(1974).
RN [8]
RP ACTIVE SITE.
RX MEDLINE=76190154; PubMed=5453;
RA Hartman F.C., Brown J.P.;
RT "Affinity labeling of a previously undetected essential lysyl residue
RT in class I fructose bisphosphate aldolase.";
RL J. Biol. Chem. 251:3057-3062(1976).
RN [9]
RP SUBSTRATE-BINDING SITE.
RX MEDLINE=80046697; PubMed=499203;
RA Patthy L., Varadi A., Thesz J., Kovacs K.;
RT "Identification of the C-1-phosphate-binding arginine residue of
RT rabbit-muscle aldolase. Isolation of 1,2-cyclohexanedione-labeled
RT peptide by chemisorption chromatography.";
RL Eur. J. Biochem. 99:309-313(1979).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=97143309; PubMed=8989320;
RA Blom N., Sygusch J.;
RT "Product binding and role of the C-terminal region in class I D-
RT fructose 1,6-bisphosphate aldolase.";
RL Nat. Struct. Biol. 4:36-39(1997).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 2-344 IN COMPLEX WITH
RP SUBSTRATE, AND MUTAGENESIS OF GLU-34; ARG-42; LYS-146 AND ARG-303.
RX MEDLINE=99435739; PubMed=10504235; DOI=10.1021/bi9828371;
RA Choi K.H., Mazurkie A.S., Morris A.J., Utheza D., Tolan D.R.,
RA Allen K.N.;
RT "Structure of a fructose-1,6-bis(phosphate) aldolase liganded to its
RT natural substrate in a cleavage-defective mutant at 2.3 Å.";
RL Biochemistry 38:12655-12664(1999).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.46 ANGSTROMS), AND MUTAGENESIS OF GLU-187;
RP GLU-189 AND LYS-229.
RX MEDLINE=21883945; PubMed=11779856; DOI=10.1074/jbc.M107600200;
RA Maurady A., Zdanov A., de Moissac D., Beaudry D., Sygusch J.;
RT "A conserved glutamate residue exhibits multifunctional catalytic
RT roles in D-fructose-1,6-bisphosphate aldolases.";
RL J. Biol. Chem. 277:9474-9483(2002).
CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
CC phosphate + D-glyceraldehyde 3-phosphate.
CC -!- PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-
CC phosphate and glycerone phosphate from D-glucose: step 4.
CC -!- SUBUNIT: Tetramer of nearly identical chains, alpha and beta,
CC which differ at only 1 position.
CC -!- PTM: Asn-360 in the alpha chain is deaminated in the beta chain.
CC -!- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
CC glycolytic enzyme are found, aldolase A in muscle, aldolase B in
CC liver and aldolase C in brain.
CC -!- MISCELLANEOUS: Alkylation of Arg-42 inactivates the enzyme.
CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase

CC family.
 CC -!- DATABASE: NAME=Worthington enzyme manual;
 CC WWW="http://www.worthington-biochem.com/ALD/".
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 DR EMBL; K02300; AAA31156.1; -; mRNA.
 DR EMBL; V00876; CAA24245.1; -; mRNA.
 DR EMBL; V00877; CAA24246.1; -; mRNA.
 DR PIR; A92444; ADRBA.
 DR PDB; 1ADO; X-ray; A/B/C/D=1-363.
 DR PDB; 1EWD; X-ray; A/B/C/D=1-363.
 DR PDB; 1EWE; X-ray; A/B/C/D=1-363.
 DR PDB; 1EWG; X-ray; A/B/C/D=1-363.
 DR PDB; 1EX5; X-ray; A/B/C/D=1-363.
 DR PDB; 1J4E; X-ray; A/B/C/D=1-363.
 DR PDB; 1ZAH; X-ray; A/B/C/D=1-363.
 DR PDB; 1ZAI; X-ray; A/B/C/D=1-363.
 DR PDB; 1ZAJ; X-ray; A/B/C/D=1-363.
 DR PDB; 1ZAL; X-ray; A/B/C/D=1-363.
 DR PDB; 6ALD; X-ray; A/B/C/D=1-363.
 DR LinkHub; P00883; -.
 DR InterPro; IPR000741; Aldolase_I.
 DR PANTHER; PTHR11627; Aldolase_I; 1.
 DR Pfam; PF00274; Glycolytic; 1.
 DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 KW 3D-structure; Direct protein sequencing; Glycolysis; Lyase;
 KW Phosphorylation; Schiff base.
 FT INIT_MET 0 0
 FT CHAIN 1 363 Fructose-bisphosphate aldolase A.
 FT /FTId=PRO_0000216938.
 FT ACT_SITE 187 187 Proton acceptor.
 FT ACT_SITE 229 229 Schiff-base intermediate with
 dihydroxyacetone-P.
 FT BINDING 42 42 Substrate; C6 phosphate group.
 FT BINDING 303 303 Substrate; C6 phosphate group.
 FT SITE 72 72 Essential for substrate cleavage.
 FT SITE 107 107 Essential for substrate cleavage.
 FT SITE 146 146 Alkylation inactivates the enzyme.
 FT SITE 361 361 Alkylation inactivates the enzyme;
 FT essential for the subsequent hydrolysis
 of the dihydroxyacetone Schiff base.
 FT SITE 363 363 Necessary for preference for fructose
 1,6-bisphosphate over fructose 1-
 phosphate.
 FT MOD_RES 203 203 Phosphotyrosine (By similarity).
 FT MOD_RES 360 360 Deamidated asparagine (in beta chain).
 FT MUTAGEN 34 34 E->A: Reduces activity 14-fold.
 FT MUTAGEN 42 42 R->A: Reduces activity 14-fold.
 FT MUTAGEN 146 146 K->A: Loss of activity.
 FT MUTAGEN 187 187 E->A: Reduces activity over 100-fold.
 FT MUTAGEN 187 187 E->Q: Reduces activity over 1000-fold.
 FT MUTAGEN 189 189 E->Q: Reduces activity 20-fold.
 FT MUTAGEN 229 229 K->M: Loss of activity.
 FT MUTAGEN 303 303 R->A: Reduces activity 400-fold.
 FT CONFLICT 34 34 E -> Q (in Ref. 3).
 FT CONFLICT 273 275 GQS -> SQE (in Ref. 5).
 FT CONFLICT 275 275 S -> E (in Ref. 5).
 FT CONFLICT 293 295 KPW -> WPK (in Ref. 5).
 FT CONFLICT 353 353 S -> R (in Ref. 6).
 FT STRAND 6 7
 FT HELIX 9 22
 FT TURN 23 23
 FT TURN 25 26
 FT STRAND 28 32
 FT HELIX 36 45
 FT TURN 46 47
 FT HELIX 52 63
 FT TURN 64 64
 FT HELIX 67 72
 FT STRAND 73 78
 FT HELIX 80 83
 FT TURN 84 84
 FT STRAND 86 86

FT	TURN	88	89
FT	STRAND	90	90
FT	STRAND	92	92
FT	HELIX	93	99
FT	TURN	100	101
FT	STRAND	103	107
FT	STRAND	112	114
FT	TURN	116	117
FT	STRAND	118	120

Query Match 100.0%; Score 100; DB 1; Length 363;
 Best Local Similarity 100.0%; Pred. No. 9.5e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
 |||||||
 Db 344 PSGQAGAAASESLFISHAY 363

RESULT 2

Q9BWD9_HUMAN
 ID Q9BWD9_HUMAN PRELIMINARY; PRT; 260 AA.
 AC Q9BWD9; Q96B15;
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2004, sequence version 2.
 DT 07-FEB-2006, entry version 23.
 DE ALDOA protein (Similar to aldolase A, fructose-bisphosphate)
 DE (Fragment).
 GN Name=ALDOA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marras M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- INTERACTION:
 CC Q86WS7:XRN1; NbExp=1; IntAct=EBI-373607, EBI-372406;
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
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 CC -----
 DR EMBL; BC000367; AAH00367.2; -; mRNA.
 DR EMBL; BC016170; AAH16170.1; -; mRNA.

DR HSSP; P04075; 1ALD.
 DR SMR; Q9BWD9; 1-260.
 DR IntAct; Q9BWD9; -.
 DR Ensembl; ENSG00000149925; Homo sapiens.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR InterPro; IPR000741; Aldolase_I.
 DR PANTHER; PTHR11627; Aldolase_I; 1.
 DR Pfam; PF00274; Glycolytic; 1.
 DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
 KW Glycolysis; Lyase.
 FT NON_TER 1 1
 SQ SEQUENCE 260 AA; 27898 MW; 861B9CDE0F1F2784 CRC64;

 Query Match 99.0%; Score 99; DB 2; Length 260;
 Best Local Similarity 95.0%; Pred. No. 9.7e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 PSGQAGAAASESLFISNHAY 20
 |||||||:|||||:|||||
 Db 241 PSGQAGAAASESLFVSNHAY 260

RESULT 3
 ALDOA_HUMAN
 ID ALDOA_HUMAN STANDARD; PRT; 363 AA.
 AC P04075; Q6FH76;
 DT 01-NOV-1986, integrated into UniProtKB/Swiss-Prot.
 DT 01-APR-1988, sequence version 1.
 DT 07-FEB-2006, entry version 74.
 DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)
 DE (Lung cancer antigen NY-LU-1).
 GN Name=ALDOA; Synonyms=ALDA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=85306986; PubMed=3840020;
 RA Sakakibara M., Mukai T., Hori K.;
 RT "Nucleotide sequence of a cDNA clone for human aldolase: a messenger
 RNA in the liver.";
 RL Biochem. Biophys. Res. Commun. 131:413-420(1985).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87161904; PubMed=3030757;
 RA Izzo P., Costanzo P., Lupo A., Rippa E., Borghese A.M., Paoletta G.,
 RA Salvatore F.;
 RT "A new human species of aldolase A mRNA from fibroblasts.";
 RL Eur. J. Biochem. 164:9-13(1987).
 RN [3]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=88183272; PubMed=3355497;
 RA Freemont P.S., Dunbar B., Fothergill-Gilmore L.A.;
 RT "The complete amino acid sequence of human skeletal-muscle fructose-
 bisphosphate aldolase.";
 RL Biochem. J. 249:779-788(1988).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=88271327; PubMed=3391172;
 RA Izzo P., Costanzo P., Lupo A., Rippa E., Paoletta G., Salvatore F.;
 RT "Human aldolase A gene. Structural organization and tissue-specific
 RT expression by multiple promoters and alternate mRNA processing.";
 RL Eur. J. Biochem. 174:569-578(1988).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91153319; PubMed=1999195;
 RA Mukai T., Arai Y., Yatsuki H., Joh K., Hori K.;
 RT "An additional promoter functions in the human aldolase A gene, but
 RT not in rat.";
 RL Eur. J. Biochem. 195:781-787(1991).
 RN [6]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry
vector (pDONR201).";
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
RC TISSUE=Cervix, Eye, Lung, Testis, and Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP PROTEIN SEQUENCE OF 1-62 AND 147-357.
RX MEDLINE=84126818; PubMed=6696436;
RA Freemont P.S., Dunbar B., Fothergill L.A.;
RT "Human skeletal-muscle aldolase: N-terminal sequence analysis of CNBr-
RT and o-iodosobenzoic acid-cleavage fragments.";
RL Arch. Biochem. Biophys. 228:342-352(1984).
RN [9]
RP NUCLEOTIDE SEQUENCE OF 1-107.
RX MEDLINE=88155643; PubMed=3441006;
RA Maire P., Gautron S., Hakim V., Gregori C., Mennecier F., Kahn A.;
RT "Characterization of three optional promoters in the 5' region of the
RT human aldolase A gene.";
RL J. Mol. Biol. 197:425-438(1987).
RN [10]
RP PROTEIN SEQUENCE OF 1-21.
RC TISSUE=Platelet;
RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
RA Thomas G.R., Vandekerckhove J.;
RT "Exploring proteomes and analyzing protein processing by mass
RT spectrometric identification of sorted N-terminal peptides.";
RL Nat. Biotechnol. 21:566-569(2003).
RN [11]
RP NUCLEOTIDE SEQUENCE OF 138-363.
RX MEDLINE=88046782; PubMed=3674018;
RA Tolan D.R., Niclas J., Bruce B.D., Lebo R.V.;
RT "Evolutionary implications of the human aldolase-A, -B, -C, and -
RT pseudogene chromosome locations.";
RL Am. J. Hum. Genet. 41:907-924(1987).
RN [12]
RP PHOSPHORYLATION SITE TYR-203, AND MASS SPECTROMETRY.
RX PubMed=15592455; DOI=10.1038/nbt1046;
RA Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT "Immunoaffinity profiling of tyrosine phosphorylation in cancer
RT cells.";
RL Nat. Biotechnol. 23:94-101(2005).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=90242948; PubMed=2335208; DOI=10.1016/0014-5793(90)80211-Z;
RA Gamblin S.J., Cooper B., Millar J.R., Davies G.J., Littlechild J.A.,
RA Watson H.C.;
RT "The crystal structure of human muscle aldolase at 3.0-A resolution.";
RL FEBS Lett. 262:282-286(1990).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=91278081; PubMed=2056525;
 RA Gamblin S.J., Davies G.J., Grimes J.M., Jackson R.M.,
 RA Littlechild J.A., Watson H.C.;
 RT "Activity and specificity of human aldolases.";
 RL J. Mol. Biol. 219:573-576(1991).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=99156067; PubMed=10048322;
 RA Dalby A., Dauter Z., Littlechild J.A.;
 RT "Crystal structure of human muscle aldolase complexed with fructose
 1,6-bisphosphate: mechanistic implications.";
 RL Protein Sci. 8:291-297(1999).
 RN [16]
 RP VARIANT HEMOLYTIC ANEMIA GLY-128.
 RX MEDLINE=88068641; PubMed=2825199;
 RA Kishi H., Mukai T., Hirono A., Fujii H., Miwa S., Hori K.;
 RT "Human aldolase A deficiency associated with a hemolytic anemia:
 RT thermolabile aldolase due to a single base mutation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8623-8627(1987).
 RN [17]
 RP VARIANT HEMOLYTIC ANEMIA GLY-128.
 RX MEDLINE=91035340; PubMed=2229018;
 RA Takasaki Y., Takahashi I., Mukai T., Hori K.;
 RT "Human aldolase A of a hemolytic anemia patient with Asp-128-->Gly
 RT substitution: characteristics of an enzyme generated in E. coli
 RT transfected with the expression plasmid pHAAD128G.";
 RL J. Biochem. 108:153-157(1990).
 CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
 CC phosphate + D-glyceraldehyde 3-phosphate.
 CC -!- PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-
 CC phosphate and glycerone phosphate from D-glucose: step 4.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- DISEASE: Defects in ALDOA are a cause of hemolytic anemia
 CC [MIM:103850].
 CC -!- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
 CC glycolytic enzyme are found, aldolase A in muscle, aldolase B in
 CC liver and aldolase C in brain.
 CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
 CC family.
 CC -----
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 CC -----
 DR EMBL; M11560; AAA51690.1; -; mRNA.
 DR EMBL; X05236; CAA28861.1; -; mRNA.
 DR EMBL; X12447; CAA30979.1; ALT_SEQ; Genomic_DNA.
 DR EMBL; CR541880; CAG46678.1; -; mRNA.
 DR EMBL; BC004333; AAHO4333.1; -; mRNA.
 DR EMBL; BC010660; AAH10660.1; -; mRNA.
 DR EMBL; BC012880; AAH12880.1; -; mRNA.
 DR EMBL; BC013614; AAH13614.1; -; mRNA.
 DR EMBL; BC015888; AAH15888.1; -; mRNA.
 DR EMBL; BC016800; AAH16800.1; -; mRNA.
 DR EMBL; X06352; CAA29654.1; -; Genomic_DNA.
 DR EMBL; M21190; AAA51697.1; -; mRNA.
 DR PIR; S14084; ADHUA.
 DR PDB; 1ALD; X-ray; @=1-363.
 DR PDB; 2ALD; X-ray; A=1-363.
 DR PDB; 4ALD; X-ray; @=1-363.
 DR IntAct; P04075; -.
 DR SWISS-2DPAGE; P04075; HUMAN.
 DR Aarhus/Ghent-2DPAGE; 1302; NEPHGE.
 DR OGP; P04075; -.
 DR Siena-2DPAGE; P04075; -.
 DR Ensembl; ENSG00000149925; Homo sapiens.
 DR H-InvDB; HIX0012935; -.
 DR HGNC; HGNC:414; ALDOA.
 DR MIM; 103850; gene+phenotype.
 DR Reactome; P04075; -.
 DR LinkHub; P04075; -.
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; TAS.
 DR GO; GO:0006000; P:fructose metabolism; TAS.
 DR GO; GO:0006096; P:glycolysis; TAS.

Query Match 99.0%; Score 99; DB 1; Length 363;
 Best Local Similarity 95.0%; Pred. No. 1.4e-07;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||:
Db 344 PSGQAGAAASESLFVSNHAY 363

RESULT 4
Q6FI10_HUMAN
ID Q6FI10_HUMAN PRELIMINARY; PRT; 364 AA.
AC Q6FI10;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Fructose-bisphosphate aldolase.
GN Name=ALDOA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC -----
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CC -----
DR EMBL; CR536528; CAG38765.1; -; mRNA.
DR SMR; Q6FI10; 2-364.
DR Ensembl; ENSG00000149925; Homo sapiens.
DR GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO:0016829; F:lyase activity; IEA.
DR GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR PANTHER; PTHR11627; Aldolase_I; 1.
DR Pfam; PF00274; Glycolytic; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Lyase.
SQ SEQUENCE 364 AA; 39420 MW; OAAED80F755A7BE8 CRC64;

Query Match 99.0%; Score 99; DB 2; Length 364;
Best Local Similarity 95.0%; Pred. No. 1.4e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||:
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 5
Q5NVR5_PONPY
ID Q5NVR5_PONPY PRELIMINARY; PRT; 364 AA.
AC Q5NVR5;
DT 04-JAN-2005, integrated into UniProtKB/TrEMBL.
DT 04-JAN-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Fructose-bisphosphate aldolase.
GN Name=DKFZp470J0811;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.;
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

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CC -----
DR EMBL; CR925940; CAI29598.1; -; mRNA.
DR SMR; Q5NVR5; 2-364.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase I.
DR PANTHER; PTHR11627; Aldolase_I; 1.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Hypothetical protein; Lyase.
SQ SEQUENCE 364 AA; 39448 MW; 4DAED62BFE37CD33 CRC64;

Query Match 99.0%; Score 99; DB 2; Length 364;
Best Local Similarity 95.0%; Pred. No. 1.4e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 6
ALDOA_MOUSE
ID ALDOA_MOUSE STANDARD; PRT; 363 AA.
AC P05064;
DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1988, sequence version 1.
DT 21-FEB-2006, entry version 59.
DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)
(Aldolase 1).
GN Name=Aldoa; Synonyms=Aldol;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129;
RX MEDLINE=88096598; PubMed=3697100;
RA Mestek A., Stauffer J., Tolan D.R., Ciejk-Baez E.;
RT "Sequence of a mouse brain aldolase A cDNA.";
RL Nucleic Acids Res. 15:10595-10595(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 1-265 AND 294-363.
RX MEDLINE=90307699; PubMed=2365699;
RA Stauffer J.K., Colbert M.C., Ciejk-Baez E.;
RT "Nonconservative utilization of aldolase A alternative promoters.";
RL J. Biol. Chem. 265:11773-11782(1990).

RN [4]
 RP NUCLEOTIDE SEQUENCE OF 98-354.
 RX MEDLINE=86192445; PubMed=3009179;
 RA Paoletta G., Buono P., Mancini P., Izzo P., Salvatore F.;
 RT "Structure and expression of mouse aldolase genes. Brain-specific
 RT aldolase C amino acid sequence is closely related to aldolase A.";
 RL Eur. J. Biochem. 156:229-235(1986).
 CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
 CC phosphate + D-glyceraldehyde 3-phosphate.
 CC -!- PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-
 CC phosphate and glycerone phosphate from D-glucose: step 4.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
 CC glycolytic enzyme are found, aldolase A in muscle, aldolase B in
 CC liver and aldolase C in brain.
 CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
 CC family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; X03797; CAA27423.1; -; mRNA.
 DR EMBL; BC043026; AAH43026.1; -; mRNA.
 DR EMBL; BC050896; AAH50896.1; -; mRNA.
 DR EMBL; J05517; AAA37210.2; -; Genomic_DNA.
 DR EMBL; Y00516; CAA68571.1; -; mRNA.
 DR PIR; S06323; ADMSA.
 DR HSSP; P00883; 1ADO.
 DR SMR; P05064; 1-363.
 DR IntAct; P05064; -.
 DR SWISS-2DPAGE; P05064; MOUSE.
 DR Ensembl; ENSMUSG00000030695; Mus musculus.
 DR MGI; MGI:87994; Aldoa.
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IDA.
 DR InterPro; IPR000741; Aldolase_I.
 DR PANTHER; PTHR11627; Aldolase_I; 1.
 DR Pfam; PF00274; Glycolytic; 1.
 DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 KW Glycolysis; Lyase; Phosphorylation; Schiff base.
 FT INIT_MET 0 0
 FT CHAIN 1 363 Fructose-bisphosphate aldolase A.
 FT /FTId=PRO_0000216937.
 FT ACT_SITE 187 187 Proton acceptor (By similarity).
 FT ACT_SITE 229 229 Schiff-base intermediate with
 FT dihydroxyacetone-P.
 FT BINDING 55 55 Substrate; C1 phosphate group.
 FT BINDING 146 146 Substrate; C1 phosphate group.
 FT SITE 363 363 Necessary for preference for fructose
 FT 1,6-bisphosphate over fructose 1-
 FT phosphate.
 FT MOD_RES 203 203 Phosphotyrosine (By similarity).
 FT CONFLICT 280 280 S -> C (in Ref. 4).
 SQ SEQUENCE 363 AA; 39225 MW; 62D27089F284BF74 CRC64;

 Query Match 97.0%; Score 97; DB 1; Length 363;
 Best Local Similarity 95.0%; Pred. No. 3e-07;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 PSGQAGAAASESLFISHAY 20
 ||||:|||||:|||||:
 Db 344 PSGQSGAAASESLFISHAY 363

RESULT 7
 ALDOA_RAT
 ID ALDOA_RAT STANDARD; PRT; 363 AA.
 AC P05065; Q63038;
 DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
 DT 13-AUG-1987, sequence version 1.
 DT 07-FEB-2006, entry version 54.
 DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase).
 GN Name=Aldoa;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86140113; PubMed=3753977;
 RA Mukai T., Joh K., Arai Y., Yatsuki H., Hori K.;
 RT "Tissue-specific expression of rat aldolase A mRNAs. Three molecular
 RT species differing only in the 5'-terminal sequences.";
 RL J. Biol. Chem. 261:3347-3354(1986).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86083188; PubMed=2416636; DOI=10.1016/0378-1119(85)90102-7;
 RA Joh K., Mukai T., Yatsuki H., Hori K.;
 RT "Rat aldolase A messenger RNA: the nucleotide sequence and multiple
 RT mRNA species with different 5'-terminal regions.";
 RL Gene 39:17-24(1985).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=87060996; PubMed=3783705;
 RA Joh K., Arai Y., Mukai T., Hori K.;
 RT "Expression of three mRNA species from a single rat aldolase A gene,
 RT differing in their 5' non-coding regions.";
 RL J. Mol. Biol. 190:401-410(1986).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
 RC TISSUE=Prostate;
 RG NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE OF 323-355, AND TISSUE SPECIFICITY.
 RC STRAIN=Donryu; TISSUE=Hepatoma;
 RX MEDLINE=84261525; PubMed=6086339;
 RA Tsutsumi R., Tsutsumi K., Numazaki M., Ishikawa K.;
 RT "Two different aldolase A mRNA species in rat tissues.";
 RL Eur. J. Biochem. 142:161-164(1984).
 CC --!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
 phosphate + D-glyceraldehyde 3-phosphate.
 CC --!- PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-
 phosphate and glycerone phosphate from D-glucose: step 4.
 CC --!- SUBUNIT: Homotetramer.
 CC --!- TISSUE SPECIFICITY: Expressed in muscle, brain and hepatoma cells.
 CC --!- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
 CC glycolytic enzyme are found, aldolase A in muscle, aldolase B in
 CC liver and aldolase C in brain.
 CC --!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
 CC family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; M12919; AAA40714.1; -; mRNA.
 DR EMBL; M14420; AAA40715.1; -; mRNA.
 DR EMBL; X04261; CAA27815.1; -; Genomic_DNA.
 DR EMBL; X04262; CAA27815.1; JOINED; Genomic_DNA.
 DR EMBL; X04263; CAA27815.1; JOINED; Genomic_DNA.
 DR EMBL; X04264; CAA27815.1; JOINED; Genomic_DNA.
 DR EMBL; BC064440; AAH64440.1; -; mRNA.
 DR EMBL; M28282; AAA40720.1; -; mRNA.
 DR PIR; A24532; ADRTA.
 DR HSSP; P00883; 1ADO.
 DR SMR; P05065; 1-363.
 DR IntAct; P05065; -.
 DR Rat-heart-2DPAGE; P05065; -.
 DR Ensembl; ENSRNOG00000023647; Rattus norvegicus.
 DR RGD; 2089; Aldoa.
 DR InterPro; IPRO000741; Aldolase_I.
 DR PANTHER; PTHR11627; Aldolase_I; 1.
 DR Pfam; PF00274; Glycolytic; 1.
 DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 KW Glycolysis; Lyase; Phosphorylation; Schiff base.
 FT INIT_MET 0 0 By similarity.
 FT CHAIN 1 363 Fructose-bisphosphate aldolase A.
 FT /FTId=PRO_0000216939.
 FT ACT_SITE 187 187 Proton acceptor (By similarity).
 FT ACT_SITE 229 229 Schiff-base intermediate with

FT dihydroxyacetone-P.
 FT BINDING 55 55 Substrate; C1 phosphate group.
 FT BINDING 146 146 Substrate; C1 phosphate group.
 FT SITE 363 363 Necessary for preference for fructose
 1,6-bisphosphate over fructose 1-
 phosphate.
 FT MOD_RES 203 203 Phosphotyrosine (By similarity).
 FT CONFLICT 144 144 F -> S (in Ref. 2).
 FT CONFLICT 164 164 M -> V (in Ref. 2).
 FT CONFLICT 329 329 K -> Q (in Ref. 5).
 SQ SEQUENCE 363 AA; 39221 MW; 48A0468B9E3B9DB8 CRC64;

 Query Match 97.0%; Score 97; DB 1; Length 363;
 Best Local Similarity 95.0%; Pred. No. 3e-07;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 PSGQAGAAASESLFISNHAY 20
 ||||:|||||:|||||:
 Db 344 PSGQSGAAASESLFISNHAY 363

RESULT 8
 Q5FWB7_MOUSE
 ID Q5FWB7_MOUSE PRELIMINARY; PRT; 364 AA.
 AC Q5FWB7;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Aldolase 1, A isoform (Blastocyst blastocyst cDNA, RIKEN full-length
 enriched library, clone:I1C0025H06 product:Fructose-bisphosphate
 aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Aldolase 1), full
 insert sequence) (NOD-derived CD11c +ve dendritic cells cDNA, RIKEN
 full-length enriched library, clone:F630015K14 product:Fructose-
 bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Aldolase
 1), full insert sequence).
 GN Name=Aldoa;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA Director MGC Project;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J, and NOD;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";

RL Methods Enzymol. 303:19-44(1999).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J, and NOD;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Henning P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabbarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J, and NOD;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J, and NOD;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [10]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC089495; AAH89495.1; -; mRNA.

Query Match 97.0%; Score 97; DB 2; Length 364;
Best Local Similarity 95.0%; Pred. No. 3e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||||||||||||
Db 345 PSGQSGAAASESLFISHAY 364

RESULT 9
Q6NY00_MOUSE
ID Q6NY00_MOUSE PRELIMINARY; PRT; 364 AA.
AC Q6NY00;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Aldolase 1, A isoform.
GN Name=Aldoa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr, and C3H/He; TISSUE=Hematopoietic Stem Cell, and
Osteoblast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RA Director MGC Project;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RA Director MGC Project;
RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; BC066801; AAH66801.1; -; mRNA.
DR EMBL; BC066218; AAH66218.1; -; mRNA.
DR HSSP; P00883; 1ADO.
DR SMR; Q6NY00; 2-364.
DR Ensembl; ENSMUSG00000030695; Mus musculus.
DR MGI; MGI:87994; Aldoa.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IDA.
DR InterPro; IPRO000741; Aldolase_I.
DR PANTHER; PTHR11627; Aldolase_I; 1.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Lyase.
SQ SEQUENCE 364 AA; 39312 MW; 5BD82BBE3E6D738A CRC64;

Query Match 97.0%; Score 97; DB 2; Length 364;
Best Local Similarity 95.0%; Pred. No. 3e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||||||||||||
Db 345 PSGQSGAAASESLFISHAY 364

RESULT 10
Q92007 CHICK
ID Q92007_CHICK PRELIMINARY; PRT; 42 AA.
AC Q92007;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Aldolase C (Aldolase A) (Fragment).
GN Name=aldolase C;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95286677; PubMed=7768978;
RA Meighan-Mantha R.L., Tolan D.R.;
RT "Noncoordinate changes in the steady-state mRNA expressed from
RT aldolase A and aldolase C genes during differentiation of chicken
RT myoblasts.";
RL J. Cell. Biochem. 57:423-431(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RA Meighan-Mantha R.L., Tolan D.R.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RA Meighan-Mantha R.L., Tolan D.R.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
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CC
DR EMBL; S78288; AAB34479.1; -; mRNA.
DR EMBL; L25374; AAA99864.1; -; mRNA.
DR EMBL; L25373; AAA48588.1; -; mRNA.
DR PIR; I51291; I51291.
DR HSSP; P00883; 6ALD.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR PANTHER; PTHR11627; Aldolase_I; 1.
DR Pfam; PF00274; Glycolytic; 1.
FT NON_TER 42 42
SQ SEQUENCE 42 AA; 4384 MW; 7E0E34B8C695DC4B CRC64;

Query Match 95.0%; Score 95; DB 2; Length 42;
Best Local Similarity 95.0%; Pred. No. 6.2e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
|||:|||||||||||||||
Db 23 PSGHAGAAASESLFISHAY 42

RESULT 11
Q4R523_MACFA
ID Q4R523_MACFA PRELIMINARY; PRT; 276 AA.
AC Q4R523;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Brain cDNA, clone: Qf1A-11254, similar to human aldolase A, fructose-
DE bisphosphate (ALDOA), transcriptvariant 2..
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15944441; DOI=10.1093/molbev/msi187;
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.;
RT "Substitution Rate and Structural Divergence of 5'UTR Evolution:
RT Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.";
RL Mol. Biol. Evol. 22:1976-1982 (2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG International consortium for macaque cDNA sequencing and analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; AB169721; BAE01802.1; -; mRNA.
DR SMR; Q4R523; 3-276.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR PANTHER; PTHR11627; Aldolase_I; 1.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
KW Glycolysis; Lyase.
SQ SEQUENCE 276 AA; 29587 MW; 2CDF4D877E140C2F CRC64;

Query Match 94.0%; Score 94; DB 2; Length 276;
Best Local Similarity 90.0%; Pred. No. 7e-07;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
||| |||||||:|||||
Db 257 PSGHAGAAASESLFVSNHAY 276

RESULT 12
Q8WNT7_MACFA
ID Q8WNT7_MACFA PRELIMINARY; PRT; 704 AA.
AC Q8WNT7;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Fructose-1,6-bisphosphate aldolase A.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
RA Terao K., Sugano S., Hashimoto K.;
RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
RT in the human genome sequence.";
RL BMC Genomics 3:36-36(2002).
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CC -----
DR EMBL; AB066558; BAB84033.1; -; mRNA.
DR HSSP; P04075; 2ALD.
DR SMR; Q8WNT7; 342-704.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR PANTHER; PTHR11627; Aldolase_I; 1.
DR Pfam; PF00274; Glycolytic; 1.

DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
 KW Glycolysis; Lyase.
 SQ SEQUENCE 704 AA; 74687 MW; 02D9A004C37DFF39 CRC64;

 Query Match 94.0%; Score 94; DB 2; Length 704;
 Best Local Similarity 90.0%; Pred. No. 1.9e-06;
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 PSGQAGAAASESLFISHAY 20
 ||| |||||:|||||
 Db 685 PSGHAGAAASESLFVSNHAY 704

RESULT 13
 Q76BG8_AMBME
 ID Q76BG8_AMBME PRELIMINARY; PRT; 331 AA.
 AC Q76BG8;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Fructose-bisphosphate aldolase A (Fragment).
 OS Ambystoma mexicanum (Axolotl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
 OC Ambystoma.
 OX NCBI_TaxID=8296;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Tail;
 RA Kikugawa K., Katoh K., Kuraku S., Sakurai H., Ishida O., Iwabe N.,
 RA Miyata T.;
 RT "Basal jawed vertebrate phylogeny inferred from multiple nuclear DNA-
 coded genes.";
 RL BMC Biol. 2:3-3(2004).
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 CC -----
 DR EMBL; AB111374; BAD17888.1; -; mRNA.
 DR HSSP; P04075; 1ALD.
 DR SMR; Q76BG8; 1-331.
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR000741; Aldolase_I.
 DR PANTHER; PTHR11627; Aldolase_I; 1.
 DR Pfam; PF00274; Glycolytic_1.
 DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 KW Glycolysis; Lyase.
 FT NON_TER 1 1
 SQ SEQUENCE 331 AA; 36170 MW; B7374F829DE6C591 CRC64;

 Query Match 89.0%; Score 89; DB 2; Length 331;
 Best Local Similarity 85.0%; Pred. No. 5.8e-06;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 PSGQAGAAASESLFISHAY 20
 ||| |||||:|||||
 Db 312 PSAQAGAAAGESLFVSNHAY 331

RESULT 14
 Q9CPQ9_MOUSE
 ID Q9CPQ9_MOUSE PRELIMINARY; PRT; 364 AA.
 AC Q9CPQ9;
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 24.
 DE Adult male testis cDNA, RIKEN full-length enriched library,
 DE clone:4933417I20 product:ALDOLASE 1, A ISOFORM homolog (Adult male
 DE testis cDNA, RIKEN full-length enriched library, clone:4921524E03
 DE product:FRUCTOSE-BISPHOSPHATE ALDOLASE A (EC 4.1.2.13) (MUSCLE-TYPE
 DE ALDOLASE) homolog) (Novel protein similar to aldolase 1, A isoform
 DE Aldol).

GN Name=Aldoa; Synonyms=RP24-191C1.1; ORFNames=RP24-191C1.1-001;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmer S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagacka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE.
RA Cobley V.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
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DR EMBL; AK016845; BAB30459.1; -; mRNA.
DR EMBL; AK014956; BAB29638.1; -; mRNA.
DR EMBL; AL928642; CAI26150.1; -; Genomic_DNA.
DR HSSP; P04075; 2ALD.
DR SMR; Q9CPQ9; 2-364.
DR Ensembl; ENSMUSG00000059343; Mus musculus.
DR MGI; MGI:87994; Aldoa.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IDA.
DR InterPro; IPR000741; Aldolase_I.
DR PANTHER; PTHR11627; Aldolase_I; 1.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Lyase.
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Query Match 88.0%; Score 88; DB 2; Length 364;
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Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISHAY 20
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RESULT 15
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ID Q9CRC1_MOUSE PRELIMINARY; PRT; 364 AA.
AC Q9CRC1;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Adult male testis cDNA, RIKEN full-length enriched library,
DE clone:4933425L11 product:fructose-bisphosphate aldolase (EC 4.1.2.13)
DE A homolog (Adult male testis cDNA, RIKEN full-length enriched library,
DE clone:1700027I20 product:fructose-bisphosphate aldolase (EC 4.1.2.13)
DE A homolog).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabavsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).

RN [3]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).

RN [4]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).

RN [5]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura M., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akihira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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 DR EMBL; AK016920; BAB30498.1; -; mRNA.
 DR EMBL; AK006425; BAB24582.1; -; mRNA.
 DR HSSP; P04075; 2ALD.
 DR SMR; Q9CRC1; 3-364.
 DR Ensembl; ENSMUSG00000063129; Mus musculus.
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR000741; Aldolase_I.
 DR PANTHER; PTHR11627; Aldolase_I; 1.
 DR Pfam; PF00274; Glycolytic; 1.
 DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 KW Glycolysis; Lyase.

SQ SEQUENCE 364 AA; 39371 MW; 0360CD12B8509A0D CRC64;
Query Match 88.0%; Score 88; DB 2; Length 364;
Best Local Similarity 85.0%; Pred. No. 9.4e-06;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Db 345 PSNESGAAASESLFISHAY 364

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